

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..65
id H75454
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 230..307
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AACTTCCAAG TTGTAGTGTT GTTGTTTTCA GCCTGCTGCT GCTGCTGCTA TTGCGGCTAG   60
GGGAACCGTC GTGGGAAGG ATGGTGTGCG AAAAATGTGA AAAGAACTT GSTACTGTTA   120
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC   180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA   238
                                         Met Glu Glu
                                         -25

WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG   285
Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
      -20                      -15                      -10

GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA   334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
      -5                      1                      5

TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG   382
Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
      10                      15                      20                      25

TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC   430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
      30                      35                      40

TAT GTT GAA TTT TCA AGG CAT AGA TGT   480
Tyr Leu Glu Phe Ser Arg His Arg Cys
      45                      50

```

(xi) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 119..361
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..120
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 124..260
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..125
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 251..309
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..343
id N40141
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 24..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..102
id N40141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 122..326
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..123
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..367)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 112..354
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(73..125)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 353..405
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LXXVVAFWAFGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATTCTTTCTT GSCCAAGGCTC TCTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTT 60
TAGGATGAG TGCACGASTG AGATCAAGAT CCAGAGGAAG AGGAG ATG GTC AGG ATG 117

-10

-5

1

GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA	213
Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu	
5 10 15	
GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA	261
Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu	
20 25 30 35	
ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA	309
Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val	
40 45 50	
AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA	357
Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala	
55 60 65	
GGA GAT GGG CCA TTG	372
Gly Asp Gly Pro Leu	
70	

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 273..433
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 133..236
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136
id AA100750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..347
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 355..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..395
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 400..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 394..423
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 5..245
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 239..337
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 244..342
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq PIVRLLSCEGTVA/KD

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 347

	-35	-30	-25	
CTG TGT GCC CGG AGA AGA ACT CGA GTC CAG CGG CCT ATC GTC AGG CTT				99
Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu				
	-20	-15	-10	
TTG AGT TGC CCA GGA ACT GTG GCC AAA GAC CTT AGG AGA GAC GAG CAG				147
Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln				
	-5	1	5	
CCT TCA GGG AGC GTG GAG ACA GGC TTT GAA GAC AAG ATT CCC AAA AGG				195
Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg				
	10	15	20	
AGA TTC TCG GAG ATG CAA AAT GAA AGA CGA GAA CAG GCA CAG CGG ACT				243
Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr				
	25	30	35	40
GTT TTA ATA CAT TGC CCA GAG AAA ATC AGT GAA AAC AAG TTT CKK AAA				291
Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys				
	45	50	55	
TAT TTA TCC CAA TTT GGA CCT ATT AAT AAT CAT TTC TTC TAT GAA AGC				339
Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser				
	60	65	70	
TTT GGT CTC TAT GCT GTC GTA GAA TTT TGC CAA AAG GAA AGC ATA GGT				387
Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly				
	75	80	85	
TCA CTG CAG AAT GGG ACT CAT ACT CCA AGC ACG GCC ATG GAG ACT GCA				435
Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala				
	90	95	100	
ATT CCA TTC AGA TCA CGT TCT TCA				459
Ile Pro Phe Arg Ser Arg Ser Ser				
	105	110		

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 43..253
id AA017309

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..124
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 28..59
 id AA017309
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(126..250)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..125
 id T52392
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 21..200
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq LVILSLKSQTLDA/ET

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AGTAAGTCCC CCGCCTCGC ATG ATG GCT GCG GTG CCG CCG GGC CTG GAG CCG      53
      Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
      -60                      -55                      -50

TGG AAC CGT GTG AGA ATC CCT AAG GCG GGG AAC CGC AGC GCA GTG ACA      101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
      -45                      -40                      -35

GTG CAG AAC CCG GGC GCG GCC CTT GAC CTT TGC ATT GCA GGT GTA ATT      149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
      -30                      -25                      -20

AAA GAA TGC CAT CTC GTC ATA CTG TCG CTG AAG AGC CAA ACC TTA GAT      197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
      -15                      -10                      -5

GCA GAA ACA GAT GTG TTA TGT GCA GTC CTT TAC AGC AAT CAC AAC AGA      245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
      1                      5                      10                      15

ATG GGC CCG CAC AAA CCG CAT TTG GCC CTC AAA CAG GTT GAG CAA TGT      293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
      20                      25                      30

TTA AAG GGT TTG ARA AAC ATG AAT TTG GAG GGC GGC      329
Leu Lys Arg Leu Xaa Asn Met Asn Leu Glu Gly Gly
      35                      40

```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 39..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..347
 id AA023764
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 146..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 145..384
 id C03036
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 11..80
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 2..71
 id C03036
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 39..231
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..193
 id R08519
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 232..302
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 193..263
 id R08519
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 11..109

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8

seq SLVHLLCQNQVLG/NP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

AAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA      49
Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly
          -30                      -25

GAG TCA GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT      97
Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn
-20          -15                      -10          -5

CAA GTG CTG GSA AAT CCA TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC      145
Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val
          1                      5                      10

AGA GTK CAT GAT TAC AAA GAA GGA ACC CCA GAA GAG AAG ACC TAC TAC      193
Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr
          15                      20                      25

ATA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC AGC GTG      241
Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val
          30                      35                      40

AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATW NYC      289
Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa
          45                      50                      55                      60

GTA CAC GAC TTA ACV SAT GGG AAG TCC TCC CAA AAM TTG CGN CGT TGG      337
Val His Asp Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp
          65                      70                      75

TCA TTG GAA GGT CTC AAC AGS GAT TTG GTG CCA ACT GSA GTC TTG GTG      385
Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val
          80                      85                      90

```

(2) INFORMATION FOR SEQ ID NO: 228:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(E) TISSUE TYPE: Brain

(4) FEATURE:

(1) NAME (KEY): cDNA

id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 219..253
id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..185
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 184..218
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 178..212
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..173
id HUM030E11B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..127
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 118..244
id AA280273
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```

GCGTCCGCGC CATCAGGCCG GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC      58
                                     Met Val Phe
                                     -30

CCT GCG AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG      106
Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp
      -25                      -20                      -15

GCG TTT TCC TGC GGC ACT TGG CTG CCG AGC CGA GCC GAA TGG CTG CTK      154
Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu
      -10                      -5                      1

RCA GTG CGA TCG ATT CAG CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC      202
Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe
      5                      10                      15                      20

GTC TTT GCC CGG GAC GGT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA      250
Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile
      25                      30                      35

AGG AAA TTA GTT GCA GAG AAT CGA      274
Arg Lys Leu Val Ala Glu Asn Arg
      40

```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrenals

(vii) FEATURE:

id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 18..115
id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 71..189
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..81
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..83
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 71..139
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 140..190
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..208
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 92..189
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..92
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 141..179
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

ACTTTCCTCAA G ATG GCG TCG AAG ATA GGT TCG AGA CGG TGG ATG TTG CAG      50
      Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln
      -25                      -20                      -15

CTG ATC ATG CAG TTG GGT TCG GTG CTG CTC ACA CGG TCG GGC TTT TGG      98
Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
-10                      -5                      1

GGC TCG TTG AGC CAG CTC ATG CTG TAC GCT GAG AGG GCT GAG GCA CGC      146
Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
5                      10                      15

GGG AAG GCG GAG ATC GCA GTG CCT TAC CTG TAT TTC ACC ATG GGG GCA      194
Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..272
id W52056
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAGAACTGCG TCTCGCGACC CAGGCGCGGG TTCCCGGAGG ACAGCCACCA AGCGATGCTG    60
CCGCCGCCGT TTCTGATTG GTTGTGGGTG GCTACCTCTT CGTTCTGATT GGCCGCTAGT   120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG   169
    Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
        -30                -25                -20

GAG AAG GAA CDT CTG GCA GTC GAC TCC TGG TGG CTA GAT CCT GGC CAC   217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
    -15                -10                -5

GCA GCG GTG GCA CAG GCA CCC CCG GCC GTG GCC TCT AGC TCC CTC TTT   265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
    1                5                10                15

GAC CTC TCA GTG CTC AAG CTC CAC CAC AGC CGC GGG   301
Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly
        20                25

```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 88..277
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 36..89
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 345..379
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..38
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 313..344
id W02951
est

(D) OTHER INFORMATION: identity 94
region 279..312
id W02951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 81..293
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 292..363
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..367
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 28..31
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 79..367
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..80
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..81
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 221..366
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 282..329
(C) IDENTIFICATION METHOD: Von Neimann matrix
(D) OTHER INFORMATION: score 4.7
seq SLAAPLTLLGHNG/LG

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

AAGGAACGAG ATGSCSGTTC TGTGGAGGCT GAGTGCCGTT TCGCGTGCCC TAGGAGGCCG 60
AGCTGTGTTG GTTCGAAC TCAGTGCTCAG AMCCTGCTCA TATCTCAGCA TTTCTTCAGG 120

TGGGTCTGCT TCCGGCTGCT TATTTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296
Met Asp Tyr Ser Leu
-15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT 344
Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val
-10 -5 1 5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT 380
Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala
10 15

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 123..338
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..134
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 339..399
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 407..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 397..435
id HUM080D04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 127..263
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..133
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 263..338
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 339..378
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 354..403
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 127..338
id HUM170H02B
est

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..134
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..397
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 339..388
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 407..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 396..426
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..299
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 135..296
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..141
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 292..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 290..346
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 402..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 407..446
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 94..282
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 44..143
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..100
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 348..408
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 306..366
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 181..396
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq LSLXASYIFGISG/FE

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AGTTTTTCAGG ARATTTGGAA GCTGCCGCAG TAGTTGGAGT CTAAGGACTC GTGACAATCT   60
TCGGGTGCCG TTCGAGAGAA AAGGGGAGGA TGCCACTGGA GTCATCCTCT TCAATGCCAC  120
TATCCTTCCC ATCTBYBYTD RCCCTCRGTA CCACACAATA CTAACCCTTC CCCTNCTCTG  180
ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT   228
Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
    -70                      -65                      -60

GCC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA   276
Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
    -55                      -50                      -45

GCT AAG GCA GTG CCA GAA AAA TTA CAA CCA HTG CTG GAT AGT CTG GAG   324
Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
    -40                      -35                      -30                      -25

CAG CTT AGT GTG TCT GGG GCA GAC GAC CAC CTT CTA TCT TTG WGT GCC   372
Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
    -20                      -15                      -10

```

CGC AAT GAA TTT GTC AGA CAG TCG
Arg Asn Glu Phe Val Arg Gln Ser
10 15

444

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 6..366
id W31798
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..353
id AA056667
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 4..342
id AA131958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..334
id H10262
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..330
id W95790
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..427
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIVYLVVVFSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC    60
CCTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC    120
TSCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA    180
CCAAGTGTTS AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC    232
          Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
          -75                      -70

CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC    280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                      -60                      -55                      -50

CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC    328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
          -45                      -40                      -35

TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC    376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
          -30                      -25                      -20

AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC    424
Arg Trp Phe Xaa Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
          -15                      -10                      -5

AGC AGC AGT    433
Ser Ser Ser
1

```

(xii) INFORMATION FOR SEQ ID NO: 234:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 39..179
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 161..261
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 22..224
id W07092
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 140..377
id W72958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 18..255
id W24219
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 18..253
id AA040714
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..110
- (C) IDENTIFICATION METHOD: Von Haljne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVCLLPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG      56
                                   Met Trp Phe Glu
                                   -20

ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA      104
Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly
      -15                      -10                      -5

CTG GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA      152
Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys
      1                      5                      10

AGG GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG      200
Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg
      15                      20                      25                      30

CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG      245
Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 162..309
id AA017973
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 181..328
id AA021972
est

(D) OTHER INFORMATION: identity 93
region 181..328
id AA013987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 168..315
id AA014054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 184..331
id W80073
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..342
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AGTTTAGCGA CCGGACCCGA AACGGGGAAG TTGTCTTG TGAGAGAGGTT AGTAAAGCAG    60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAGTCTTAGG TGATCGAGGG TGTGCCCAGG   120
GGCGGGACTT GTTTGCGCCT CCCGTTCCCT CCCAATTTCC AAACGTGTCA CCCC GGCGCC    180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG TTC AAG CTG GAG GCT CAT CGC      231
              Met Glu Phe Lys Leu Glu Ala His Arg
              -45                               -40

ATC GTC AGC ATC TCT CTG GGC AAG ATC TAC AAC TCG CGG GTC CAG CGC      279
Ile Val Ser Ile Ser Leu Gly Lys Ile Tyr Asn Ser Arg Val Gln Arg
      -35                               -30                               -25

GGC GGC ATC AAG CTG CAT AAG AAC CTC CTG GTC TCG CTG GTG CTG CGC      327
Gly Gly Ile Lys Leu His Lys Asn Leu Leu Val Ser Leu Val Leu Arg
      -20                               -15                               -10

ASG CCC GCC AAG TCT ACC CGA GCG GGG                                354
Xaa Pro Ala Lys Ser Thr Arg Ala Gly
      -5                               1
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 179..333
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..363
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..285
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 338..381
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other

id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 27..337
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 347..382
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..216
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 271..332
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 216..278
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 332..376
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..310
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 370..414
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 311..355
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IASGLGLXLDWWT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTTC 60
GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA 114
Met Ala Val Leu Ser Lys Glu
-95

TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC 162
Tyr Gly Phe Val Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
-90 -85 -80 -75

CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG 210
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
-70 -65 -60

TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC 258
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
-55 -50 -45

TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC 306
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe
-40 -35 -30

TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT 354
Leu Phe Ile Ile Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
-25 -20 -15

GGC CTG GAT TTC DCN CTG GAT TGT TGG ACG AGT TCT TTA TGC TTA TGG 402
Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp
-10 -5 1 5

CTA TTA CAG GGG CCG GGG 420
Leu Leu Arg Gly Pro Gly

```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 28..227
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..200
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 265..310
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 238..283
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 227..263
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 201..237
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 352..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 328..361
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(259..408)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 123..272
 id N93600
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(85..207)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 325..447
id N93600
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(202..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 117..323
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(116..153)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 375..412
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(167..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 324..359
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(258..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 123..273
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(208..251)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 280..323
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(163..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 325..447

(A) NAME/KEY: other
 (B) LOCATION: complement(90..125)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 411..446
 id N93603
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..397
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq RIPS LPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

AAAAGGAAAG AGGTYSGGAG CGCTCGCGAG ATCTCGGACC ACCCAACCTG AAAGGTGCTT   60
AGGAAGTTGA AAGGCCCAGA GGAGGCCTCC GGGCAAATGG CCGGAGCTGG ACCGACCATG   120
CTGCTACGAG AAGAGAATGG CTGTTGCAGT CGGCGTCAGA GCAGCTCCAG TGCCGGGGAT   180
TCGGACGGAG AGCGCGAGGA CTCGGCGGCT GAGCGCGCCC GACAGCAGCT AGAGGCGCTG   240
CTCAACAAGA CTATGCGCAT TCGCATGACA G ATG GAC GGA CAC TGG TCG GCT       292
                               Met Asp Gly His Trp Ser Ala
                               -40

GCT TTC TCT GCA CTG ACC GTG ACT GCA ATG TCA TCC TGG GCT CGG CGC       340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                               -30                               -25                               -20

AGG AGT TCC TCA AGC CGT CGG ATT CCT TCT CTG CCG GGG AGC CCC GTG       388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
          -15                               -10                               -5

TGC TGG GCC TGG CCA TGG                                               406
Cys Trp Ala Trp Pro Trp
          1

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Liver

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 20..171
id N41898
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 38..176
id H69272
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ACTTGACAGG	CASGGAGGGC	TAGGCTGTGC	ATCCCTCCGC	TGCATTGCA	GGGAG	ATG	58
						Met	
GCT	CAG	CGA	CTT	CTT	CTG	AGG	106
Ala	Gln	Arg	Leu	Leu	Leu	Arg	
-15			-10			-5	1
AAG	CCC	TCT	CAG	GGT	CAG	TGG	154
Lys	Pro	Ser	Gln	Gly	Gln	Trp	
			5			10	15
ACC	CCA	CAA	TGC	AGT	CCT	GGT	202
Thr	Pro	Gln	Cys	Ser	Pro	Gly	
		20				25	30
CGG	ACG						208
Arg	Thr						
		35					

(2) INFORMATION FOR SEQ ID NO: 239:

1. SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

2. MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

(A) NAME/KEY: other
(B) LOCATION: 124..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 103..322
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 4..115
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..398
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 336..377
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..337
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..385
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..134
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..128
id AA054941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 191..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..277
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 117..184
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 360..397
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 97..316
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 330..371
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 108..255
id H72704
est

ix FEATURE:

- (A) NAME/KEY: other

id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(101..151)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 259..309
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(357..398)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 9..50
id H72704
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 311..385
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq FLLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

AGACGTGTTT TTCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCAAAA TGGAGCTCGA    60
GGCCATGAGC AGATATACCA GCCCAGTGAA CCCAGCTGTC TTCCCCCATC TGACCGTGGT   120
GCTTTTGGCC ATTGGCATGT TCTTCACCGC CTGGTTCTTC GTTTACGAGG TCACCTCTAC   180
CAAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT   240
GGGCTTTGGA GTCCTCTTCC TGCTGCTCTG GGTGCGCATC TACGTGTGAG CACCCAAGGG   300
TAACAACCAG ATG GCT TCA CTG AAA CCT GCT TTT GTA AAT TAC TTT TTT       349
      Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe
      -25                -20                -15

TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA       397
Leu Leu Leu Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu
      -10                -5                1

GGG
Gly
5

```

400

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 202..372
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 213..292
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 157..214

(C) IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 167..337
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155

id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 226..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 177..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..386
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
AAAAACGTCC ATRACTGAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG      60
GGGCGTGGTT GTTCGTGATC CTTGCATCTG TTACTTAGGG TCAAGGCTTG GGTCTTGCCC      120
GCGAGACCCT TGGGACGACC CGGCCCCAGC GCAST ATG AAC CTG GAG CGA GTG      173
                               Met Asn Leu Glu Arg Val
                               -75
TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG      221
Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly
-70                               -65                               -60
TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC      269
Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe
-55                               -50                               -45                               -40
GGA GAG GGC TTT TTT GTC GCA GGC TAC ACA GAA CAG ACC CAA ATC AAA      317
Arg Glu Ala Pro Leu Val Pro Ala Tyr Thr Glu Gln Ser Gln Ile Lys
-35                               -30                               -25
GGC TAT GTC TGG GGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG      365
Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val
-20                               -15                               -10
GTC ACC TCG TGG ATC ACC ATC TTC CAG ATC      395
Leu Thr Ser Thr Ile Thr Ile Phe Gln Ile
```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 170..205
id AA090974
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
ATTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGATA    60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AGT    111
           Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser
           -20                      -15                      -10

TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA    159
Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly
           -5                      1                      5

CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG                                189
His Ile Gly Val Tyr Tyr Arg Gly Gly Val
           10                      15
```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 16..262
id AA044042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 46..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..33
id AA044042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 6..239
id AA127902
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..216
id AA056679
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(104..308)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 246..450
id W93399
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..184
id H39528
est

(D) OTHER INFORMATION: score 4.4
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT   60
GGCGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG GTACACTGAT GCTGAAGTAC   120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG   169
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25                -20                -15                -10

GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC   217
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5                        1                        5

AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT CCT GAG CAA GAT   265
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
      10                15                20

AGT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG   313
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
      25                30                35

```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..232
id AA088487
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 341..409
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VFCLLSIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGTCGTTGCC ATSGATCCTG GGGACGACTG GCTGGTGGAA TCCTTGCGCT TGTAATCGT    60
ACCAGGATTT CTATGCATTC GACCTGTCAG GAGCCACTCG AGTCCTTGAA TGGATTGATG   120
ACAAAGGAGT CTTTGTGCT GGCTATGAAA GCCTGAAAAA GAATGAAATT CTTCATCTGA   180
AATTACCTCT CAGACTTTCT GTAAAGGAAA ACAAGGGCTT ATTCCCAGAA AGAGATTTCA   240
AAGTGCGCCA TGGAGGATTT TCAGACAGGT CTATCTTTGA TCTAAAGCAT GTGCCACATA   300
CCAGGTATGG TCAATTTTGT GATCCAGCCA TCCACACAGG ATG GGA TGG GAT GGC    355
                                         Met Gly Trp Asp Gly
                                         -20

TGC AAA TGC CTG GGG GTA TTC TGC CTC CTC ATC TCC ATT CCC ACC CCC    403
Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile Ser Ile Pro Thr Pro
      -15                      -10                      -5

TCA GCA CAC CTG
Ser Ala His Leu
      1

```

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..451
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 122..417
id AA085629
est

14 FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 14..114
id AA085629
est

(D) OTHER INFORMATION: identity 99
region 134..237
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..126
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 254..294
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 15..112
id H35088
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..252
id HUML11153
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..365
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq ILAHLRLGLIPIHA/DP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG	50
Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala	
-115 -110	
TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC	98
Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe	
-105 -100 -95 -90	
CCG GTA ACT ATT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY TTC	146
Pro Val Thr Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe	

	-85	-80	-75	
GAA GRA AGA AWT TTC CGT GTG GAT GTA GTA CAC ATG GAT GAA AAC TCA				194
Glu Xaa Arg Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser				
	-70	-65	-60	
CTG GAG TTT GAC ATG GTG GGA ATT GAC GCA GCC ATT GCC AAT GCT TTT				242
Leu Glu Phe Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe				
	-55	-50	-45	
CGA CGA ATT CTG CTA GCT GAG GTG CCA ACT ATG GCT GTG GAG AAG GTC				290
Arg Arg Ile Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val				
	-40	-35	-30	
CTG GTG TAC AAT AAT ACA TCC ATT GTT CAG GAT GAG ATT CTT GCT CAC				338
Leu Val Tyr Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His				
	-25	-20	-15	-10
CGT CTG GGG CTC ATT CCC ATT CAT GCT GAT CCC CGT CTT TTT GAG TAT				386
Arg Leu Gly Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr				
	-5	1	5	
CGG AAC CAA GGA GAT GAA GAA GGC ACA GAG ATA GAT ACT CTA CAG TTT				434
Arg Asn Gln Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe				
	10	15	20	
CGT CTC CAG GTC AGA TGC ACT CGG				458
Arg Leu Gln Val Arg Cys Thr Arg				
	25	30		

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(x) FEATURE:

- (a) NAME/KEY: other
- (b) LOCATION: 61..188
- (c) IDENTIFICATION METHOD: blastn
- (d) OTHER INFORMATION: identity 97
region 45..172
id AA156837
est

(y) FEATURE:

- (a) NAME/KEY: other

id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 172..239
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..49
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..206
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 236..318
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 207..241
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 44..209
id AA181144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 235..317
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..48
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 225..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 209..240
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 185..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 169..318
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 46..169
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..205
est

(B) LOCATION: 252..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: . identity 90
 region 236..318
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 341..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 323..362
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 221..256
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 206..241
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 12..242
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq FEARIALLLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATACTGCGAG T ATG GCG GCG TCA AAG GTG AAA CAG GAC ATG CCT CCG CCG	50
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro	
-75 -70 -65	
GGG GGC TAT GGG CCG ATC GAC TAC AAA CGG AAC TTR CCG CGT CGA GGA	98
Gly Gly Tyr Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly	
-60 -55 -50	
CTG TCG GGC TAC AGC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC	146
Leu Ser Gly Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr	
-45 -40 -35	
GGG CAC TGG AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA	194
Gly His Trp Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln	
-30 -25 -20	
ATC GAG GAC TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA	242
Ile Glu Asp Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala	
-15 -10 -5	
GAA ACC GAC CGG ARG ACC TTG CAG ATG CTT CGG GAG AAC CTG GAG GAG	290
Ser Thr Asp Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu	
1 5 10 15	
GAG GCG ATC ATC ATG MAG GAC GTS CYC GAC TGG AAS GTG GGG RAA KVV	338
Glu Ala Ile Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa	

	20		25		30		383
GHT GTT CCA CAC AAC CCG CTG GGT GCQ CCC CTT GAT CGG GGA GCT							
Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala							
	35	*	40		45		

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..267
id AA027968
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 94..278
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..99
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..265
id HSC0SD021
est

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..259
 id T31694
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 116..274
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 61..219
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 55..107
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..53
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 273..307
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 219..253
 id R38457
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 164..289
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq VLFFGTGWWIIIDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AATGCGCGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGGCC   60
GTTTTGTTTT CTTGGCTAAA ATCGGGGGAG TGAGGCGGGC CGGCGCGGCG CGACACCGGG   120
CTCCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT   175
                               Met Ser Gly Phe
                               -40
CTA BAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC   223
Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg
      -35                      -30                      -25
AAT ACT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG   271
Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp
      -20                      -15                      -10
TGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG   310
Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr Arg

```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 73..353
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 42..71
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 145..290
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 47..145
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 391..398

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 10..45
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 225..356
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

AAGGTGCTCG TCATGCGCAA TGTGGCGCTG CGGCGGGCGG CAGGGCCTGT GTGTGCTGAG   60
GCGGCTGAGC GGCGGACATG CACACCACAG AGCGTGGCGA TGGAACAGTA ACCGGGCTTG   120
TGAGAGGGCT CTGCAGTATA AACTAGGAGA CAAGATCCAT GGATTCACCG TAAACCAGGT   180
GACATCTGTT CCGGAGCTGT TCCTGACTGC AGTGAAGCTC ACCC ATG ATG ACA CAG   236
                               Met Met Thr Gln

GAG CCA GGT ATT TAC ACC TGG CCA GAG AAA ACA CGA ATA ATC TGT TCA   284
Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg Ile Ile Cys Ser
-40                               -35                               -30                               -25

GCG TGC AGT TCC GTA CCA CTC CCA TGG ACA GTA CTG GTG TTC CTC ACA   332
Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu Val Phe Leu Thr
                               -20                               -15                               -10

TTC TTG AGC ATA CCG TCC TTT GTG GGT CTC AGA AAT ATC CGT GCA GAG   380
Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn Ile Arg Ala Glu
                               -5                               1                               5

ACC TTT CTT CAA AAT GTT   396
Thr Phe Leu Gln Asn Val
10

```

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(53..194)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 444..585
id AA161193
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(227..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 311..408
id AA161193
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 230..308
id AA161193
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(408..446)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 188..226
id AA161193
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 75..153
id R06283
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(275..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 156..205
id R06283
est

(ix) FEATURE:

(A) NAME/KEY: other

id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 286..342
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 89..141
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 242..283
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..44
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 351..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 312..367
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 371..403
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..225
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 166..198
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(171..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 313..466
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 232..310
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(408..446)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 190..228
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 39..80
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq FLTALLWRCRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC    56
                                   Met Phe Leu Thr Ala Leu
                                   -10

ATC TGG CGC GGC CGC ATT CCG GGC CGT CAG TGG ATC GGG AAG CAG CGG    104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
      -5              1              5

GGG CCG CGG TTC GTG TCG TTS CGC GGC AAG CAG AAC ATG ATC CGC CGC    152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
      10              15              20

CTT GAG ATC GAG GCG GAG AAC CAT TAC TGG CTG AGC ATG CCG TAC ATG    200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
      25              30

```

TTC GAG GCS ATA AAG GCG GCC GCC ACT TCC AAG TTC CCC CCG CAT AGA	296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg	
60 65 70	
TTC ATT GCG GAC CAG CTC GAC CAT CTC AVK VGT CAC CAA GAA ATG GTC	344
Phe Ile Ala Asp Gln Leu Asp His Leu Xaa Xaa His Gln Glu Met Val	
75 80 85	
CTA ATC CTG AGT CGT CAC CCT TGG ATT TTA TGG ATC ACG GAG CTG ACC	392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr	
90 95 100	
ATC TTT ACC TGG TCT GGA CTG AAA AAC TGT AGC TTG TGT GAA AAT GAG	440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu	
105 110 115 120	
CTT TGG ACC AGT CTT TAT	458
Leu Trp Thr Ser Leu Tyr	
125	

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..381
id W56872
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..291
id W31727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354
id W16469
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..356
id N31028
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..354
id W16470
est

(1x) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..389
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCCC/CL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTC	60
AGACCCGACC GTTATCCAGT CGGTTCTGTGG AGAGGAGAGG TGSACTTTAC AGGTCCCCG	119
ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC	167
Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala	
-90 -85 -80 -75	
CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG	215
Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly	
-70 -65 -60	
GSA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG	263
Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln	
-55 -50 -45	
TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT AAA ACC ACA GTG TAT	311
Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr	
-40 -35 -30	
GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC ACC TGC CTC	359
Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu	
-25 -20 -15	
GGG GGG TGG TGG AGG GGT GTG TGT TGG TGG TGT GTG TGG	398

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..332
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..59
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 329..368
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..273
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 274..321
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..57
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 329..368
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 318..357
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 68..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..264
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 329..368
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 261..300
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 50..249
id W57829
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 3..49
id W57829
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..235

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

AAGTTCGGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC AGG TCT      49
  Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser
                    -50                      -45

CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA CAT TCG GTG      97
Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val
  -40                      -35                      -30

CTT TTA CCT ACC TAC AAC GAG CGC GAR GAA CTG CCG CTC ATC GTG TGG     145
Leu Leu Pro Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp
  -25                      -20                      -15                      -10

CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA ATT ATA     193
Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile
                    -5                      1                      5

ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT GAA CAG     241
Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln
  10                      15                      20

TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA CGA GAG     289
Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu
  25                      30                      35

AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CAT GGA ATG RAA ACA TGC     337
Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys
  40                      45                      50                      55

CAC AGG RAA CTA CAT CAT TAT TAT GGA TGC                             367
His Arg Xaa Leu His His Tyr Tyr Gly Cys
                    60                      65

```

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..408
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 61..399
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..60
id AA114853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..391
id W23545
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 42..381
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..68
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..41
id AA069652
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 8..333
id AA084987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..409
(C) IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 303..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```

ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCC 60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC 120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTAAGTATA AGCAGCTTCG 180
GAAAGGWGCC AATGAGGCCA CCAAACCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT 240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA 300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG 347
  Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu
      -10                -5                1

CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG 395
Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys
      5                10                15

AAG GCT CGC AGC 407
Lys Ala Arg Ser
      20

```

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 34..159
id N52621
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..38

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..31
id N52621
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 5..152
id AA157163
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..66
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
ACTTCTAAG ATG GCT GCC GCT ACC GGT GCG GTG GCA GCC TCG GCC GCC TCG      51
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser
           -15                               -10

GGT CAG GCG GAA GST AAA AAG ATC ACC GAT CTG CGG GTC ATC GAT CTG      99
Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu
-5              1              5              10

AAG TCC GAG CTG AAG CGG CGG AAC TTA GAC ATC ACC GGA GTC AAG ACC      147
Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr
           15              20              25

GTG CTC ATC TCC CSA CTA AGG      168
Val Leu Ile Ser Arg Leu Arg
           30
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(B) DEVELOPMENTAL STAGE: Fetal
(C) TISSUE TYPE: Kidney

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..306
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..103
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 340..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 304..397
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..388
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..356
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..389
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 82..339
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 50..139
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..90
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 387..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 338..384
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 126..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 75..382
 id H29689
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 23..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

ATTCCTCCTG CCGTAGTAG CC ATG BCG GCC ATG AGT TTG TTG CKG CGG GTT      52
      Met Ala Ala Met Ser Leu Leu Xaa Arg Val
                        -15                      -10

TAG GTT ACT GCG GTG GCA GCT CTG TCT GGC CGG CCC GTT GGC ACY NGC      100
Ser Val Thr Ala Val Ala Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa
      -5                      1                      5

CTC GGA TTT GGG GGC TTC CTC ACT CST GGC TTT CCG AAG GCT GCT GCT      148
Leu Gly Phe Gly Gly Phe Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala
      10                      15                      20                      25

```

CCT TCT AGA TTC TAT GAC AGG CGT TTT TTG AAG TTA TTG AGA TTC TAC	244
Pro Ser Arg Phe Tyr Asp Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr	
45 50 55	
ATT GCA TTG ACT GGG ATT CCA GTA GCA WTT TTC ATA ACT CTG GTG AAT	292
Ile Ala Leu Thr Gly Ile Pro Val Ala Xaa Phe Ile Thr Leu Val Asn	
60 65 70	
GTA TTC ATT GGT CAA GCT GAA CTA GCA GAA ATT CCA GAA GGC TAT GTC	340
Val Phe Ile Gly Gln Ala Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val	
75 80 85	
CCA GAA CAC TGG GAA TAT TAT AAG CAT CCC ATA TCA AGA TGG ATT GCC	388
Pro Glu His Trp Glu Tyr Tyr Lys His Pro Ile Ser Arg Trp Ile Ala	
90 95 100 105	
CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG	433
Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met	
110 115 120	

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..452
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..409
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..54
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 107..404
id AA088577

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..100
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 29..96
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 6..41
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..36
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 7..156
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 156..279
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 46..207
id H85485
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

RI SEQUENCE DESCRIPTION: SEQ ID NO: 254:

-25	-20	-15	-10	
CGG GGC CTG CCG CGT GTG AGC CTG GCC AAC TTA AAG CCG AAT CCC GGC				156
Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly				
	-5	1	5	
TCC AAG AAA CCG GAG AGA AGA CCA AGA GGT CGG AGA AGA GGT AGA AAA				204
Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Arg Gly Arg Lys				
	10	15	20	
TGT GGC AGA GGC CAT AAA GGA GAA AGG CAA AGA GGA ACC CGG CCC CGC				252
Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg				
	25	30	35	
TTG GGC TTT GAG GGA GGC CAG ACT CCA TTT TAC ATC CGA RTC CCA AAA				300
Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys				
	40	45	50	55
TAC GGG TTT AAC GAA GGA CAT AGT TTC AGA CGC CAG TAT AAG CCT TTG				348
Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu				
	60	65	70	
AGT CTC AAT AGA CTG CAG TAT CTT ATT GAT TTG GGT CGT GTT GAT CCT				396
Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro				
	75	80	85	
AGT CAA CCT ATT GAC TTA ACC CAG CTT GTC AAT GGG AGA GGT GTG ACC				444
Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr				
	90	95	100	
ATC GCG CCG				453
Ile Ala Pro				
	105			

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..103
id T11164
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 133..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 102..192
 id T11164
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AAAGGAAGCG GCTAACT ATG GCG ACC GCC ACG GAG CAG TGG GTT CTG GTG	50
Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val	
-40 -35	
GAG ATG GTA CAG GCG CTT TAC GAG GCT CCT GCT TAC CAT CTT ATT TTG	98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu	
-30 -25 -20 -15	
GAA GGG ATT CTG ATC CTC TGG ATA ATC AGA CTT CTT TTC TCT AAG ACT	146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr	
-10 -5 1	
TAC AAA TTA CAA GAA CGA TCT GAT CTT ACA GTC AAG GAA AAA GAA GAA	194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu	
5 10 15	
CTG ATT GAA GAG TGG CAA CCA GAA CCT CTT GTT CCT CCT GTC CCA AAA	242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys	
20 25 30	
GAC CAT CCT GCT CTC AAC TAC AAC ATC GTT TCA GGC CCT CCA AGC CAC	290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His	
35 40 45 50	
AAA ACT GTG GTG AAT GGA AAA GAA TGT ATA AAC TTC GCC TCA TTT AAT	338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn	
55 60 65	
TTT CTT GGA TTG TTG GAT AAC CCT AGG GTT AAG GCA GCA GCT TTA GCA	386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala	
75 80	
TCT CTA AAG AAG TAT GGC GTG GGG ACT TGT GGA CCC TGT	425
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys	
85 90 95	

1. INFORMATION FOR SEQ ID NO: 255:

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 124..305
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..123
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..361
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..144
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 145..274
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 276..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 275..308
id H23328

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 147..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 146..308
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 69..145
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..40
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..36
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..182
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 222..258
id T62768
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..398
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCARS/FP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AAATANTGAG GCCTGGGAGC AAGAACCTGT AGGCAGCGCT TSAGGGTAGC GGGATAGCAG 60
GTGGAACGGC CGTGGGAGGC GGGGGCTCTG GGCGGAACAA AAATCACAGG ATGTCAGAGG 120
ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC 176
Met Glu Asp Pro Asn
-75

GGT GAA GGA AAG ATG AAG GAG GAG GAT TGA GCG AAG GAG ACG AAT GCG 240

Gln	Ser	Pro	Gly	Gly	Asn	Ile	Cys	His	Leu	Gly	Ala	Pro	Lys	Cys	Thr	
			-55					-50					-45			
CGC	TGC	CTC	ATC	ACC	TTC	GCA	GAT	TCC	AAG	TTS	SAG	GAG	CGT	CAC	ATG	320
Arg	Cys	Leu	Ile	Thr	Phe	Ala	Asp	Ser	Lys	Xaa	Xaa	Glu	Arg	His	Met	
		-40					-35					-30				
AAG	CGG	GAG	CAC	CCA	GCG	GAC	TTC	GTG	GCC	CAG	AAG	CTG	CAG	GGG	GTC	368
Lys	Arg	Glu	His	Pro	Ala	Asp	Phe	Val	Ala	Gln	Lys	Leu	Gln	Gly	Val	
	-25					-20					-15					
CTC	TTC	ATC	TGC	TTC	ACC	TGC	GCC	CGC	TCC	TTC	CCC	TCT				407
Leu	Phe	Ile	Cys	Phe	Thr	Cys	Ala	Arg	Ser	Phe	Pro	Ser				
-10					-5					1						

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..302
id AA062591
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..45
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 43..89
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..45
 id AA158431
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 444..490
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 43..89
 id AA158431
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 65..160
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AAGGATCCTC TACCGGCTTT TCGAGTCAGT GCTGCCGCCG CTGCCCCGGG CTTTGCAGAG    60
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG    109
  Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu
    -30                      -25                      -20

CAC TCC AAC GTG CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT    157
His Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn
   -15                      -10                      -5

AAC AAC CCT GAG TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG    205
Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val
    1                      5                      10                      15

TAT CAT GCA GAT TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG    253
Tyr His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val
    20                      25                      30

AGT AAG TAT ACC ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT AAA ACT    301
Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr
    35                      40                      45

TCA AAA GTG ASA CCT TCA ACT GGA AAT TCT GCA TCT ACT CCA CAA AGT    349
Ser Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser
    50                      55                      60

CAG TGT CTT CCA TCT GAA ATT GAA GTG AAA TAC AAA ATG GCT GAA TGT    397
Gln Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys
    65                      70                      75

TAT ACA ATG CTA AAA CAA GAT AAA GAT GCC ATT GCT ATA CTT GAT GGG    445
Tyr Thr Ala Thr Thr Thr Glu Asp Ile Asp Ile Thr Thr Thr Thr Thr Thr
  
```

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..312
id HSC26F061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 20..260
id W30546
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 66..252
id H34739
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LVVHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC 60
CTGGCCCCCTG ACACGGGCTGC ACTTTCCATC CCGTCGCGGG GCCGGCCGCT ACTCCGGCCC 120
CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169
Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val
```

-55

-50

-45

GCT	GAG	TAC	CTG	ACC	CCG	GTC	CTC	AAG	GAA	TCA	AAG	TTT	AAG	GAA	ACA	217
Ala	Glu	Tyr	Leu	Thr	Pro	Val	Leu	Lys	Glu	Ser	Lys	Phe	Lys	Glu	Thr	
			-40					-35					-30			
GGT	GTA	ATT	ACC	CCA	GAA	GAG	TTT	GTG	GCA	GCT	GGA	GAT	CAC	CTA	GTC	265
Gly	Val	Ile	Thr	Pro	Glu	Glu	Phe	Val	Ala	Ala	Gly	Asp	His	Leu	Val	
		-25					-20					-15				
CAC	CAC	TGT	CCA	ACA	TGG	CAA	TGG	GCT	ACA	GGG	GAA	GAA	TTG	AAA	GTG	313
His	His	Cys	Pro	Thr	Trp	Gln	Trp	Ala	Thr	Gly	Glu	Glu	Leu	Lys	Val	
	-10					-5				1					5	
AAG	GCA	TAC	CTA	CCA	ACA	GGC	AAA	TGG								340
Lys	Ala	Tyr	Leu	Pro	Thr	Gly	Lys	Trp								

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 89..262
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..428
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 334..402
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 401..438
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..285
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..43
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 401..444
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..345
id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 283..313
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 102..264
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 336..441
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 262..323
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 28..79
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 78..254
id H72445
est

(ix) FEATURE:

region 252..313
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..69
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 209..472
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

AGATCCCGCC TGGGGCCGCG TGAGTGGCAC TTAAGCGGGC CATGCCATGC AACCTTGGGC      60
GCTGCCAACC GTGGGCGAGC TCTGGGTGTG CGGGCGGCCT GCGCGGGCGC TCCGCTGTGT      120
CAGCGTGTTA TGATGCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTG      180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA      232
              Met Ala Thr Leu Thr Phe Ser Leu
              -85

AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG      280
Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu
-80              -75              -70              -65

TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT      328
Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala
              -60              -55              -50

GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT      376
Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala

```

[illegible]

(D) OTHER INFORMATION: identity 97
region 143..250
id R57473
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..243
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 195..298
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 243..279
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 299..335
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 97..194
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 235..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 193..233
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 80..265
id W31972
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 123..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PSLAAGLLFGSXA/GL

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

TCGCGGGGCC TTCGGCAGAT GCAGGCCTGG GGTAGTCTCC TTTCTGGACT GAGAAGAGAA 120
GA ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC 167
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
-45 -40 -35

TTT GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
-30 -25 -20

AAA ACA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTC GGC AGT 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
-15 -10 -5

VWA GGC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCA AGR AAC GTT 311
Xaa Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
1 5 10

TGG GGT TTC CTA GCC GCT ACA TCT GTT 338
Trp Gly Phe Leu Ala Ala Thr Ser Val
15 20

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..239
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..89
id R27748
est

(D) OTHER INFORMATION: identity 97
region 116..252
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..56
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..98
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 59..159
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..206
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 14..56
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 32..228
id H35655
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 102..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: .identity 90
 region 108..304
 id AA038389
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 108..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

AGGGGGTTSC GTGCTCTCT GGTAAAGGCG TGCAGGTGTT GGCCGCGGCC TGTGAGCTGG    60
GATGAGCCST GGTCCCGGTG GAAGCAAGGG GAGCCCCAGC SGGAGCC ATG GCC AGT    116
                                     Met Ala Ser
ACA GTG GTA GCA GTT GGA CTG ACC ATT GCT GGT GCA GGA TTT GCA GGC    164
Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly
-15                               -10                               -5                               1
CGT TAC GTT TTG CAA GCC ATG AAG CAT ATG GAG CBT CAA GTA AAA CAA    212
Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln Val Lys Gln
                               5                               10                               15
GTT TTT CAA AGC CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA    260
Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg
                               20                               25                               30
GGT BGG TTT GAA CCC APA ATG RCA AAA CGG GAA GCA GCG GGG    302
Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala Gly
                               35                               40                               45

```

(2) INFORMATION FOR SEQ ID NO: 262:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: cDNA

(3) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (B) TISSUE TYPE: Brain

(4) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 108..161

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..98
id T32007
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R59039
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 19..78
id R59039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 70..254
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..72
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide
(B) LOCATION: 136..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

AAAGTTCTCC TTCCACCTTC CCCACCCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT    60
GGATTCAGG CATTGCTGCA GCTGCTCCAC AGCCCTTTTC AGGACCCAAA CAACCGCAGC    120
CGCTGTTCCC CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC    171
      Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
      -80                               -75

TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA    219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-70                               -65                               -60

GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG    267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-55                               -50                               -45                               -40

AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AST CGA CCA GCG    315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
-35                               -30                               -25

GTT CAG GGG CCA CAT GGT TTT CGG TAT AAA GCA TTC TCC TTC TCT AGG    363
Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg
-20                               -15                               -10

ATG CTA TCA CAG TGG AAA GGT GAG TCC CTA AAT ATC GCG ACG AAT TTT

```

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe
10 15 20 25

TTT TTT
Phe Phe

465

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 117..274
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..116
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..355
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 270..302
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 113..311
id R59757
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 36..112
id R59757
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..41
id R59757
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..330
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..292
id R25047
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 17..93
id R25047
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 38..331
id R23993
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 163..294

(A) NAME/KEY: other
 (B) LOCATION: 132..194
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 131..193
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 305..354
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 308..357
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 350..390
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 354..394
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 243..368
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq ITSSLFLGRGSA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AAGAAGCCGG TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC   60
CGATTTGATT TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTCT GGATCCAGAC  120
CCAGGCAGCG CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCCTTGGT  180
GGAGGAAAAT AAAACACTCT GGTCTTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT  240
TC ATG AGC TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC   287
  Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala
    -40                      -35                      -30

CCT CGG ATG ATT TCC GAG GGA GAC ATA GGA GGC ATT GCT CAA ATC ACC   335
Pro Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr
   -25                      -20                      -15

TCC TCT CTA TTC CTG GGC AGA GGC AGT GTG GCC TCC AAT CGG CAC CTC   393
Ser Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu
  -10                      -5                      1                      5

CTC CAG GCT CGT GGC ATC                                           401
Leu Gln Ala Arg Gly Ile
                   10

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..183
id AA022583
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(69..228)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 281..440
id AA022584
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 66..119
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq PALCLFDVDGTLT/AP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

AGGAAGTTCC GGGCCGAGTT CCTCGTGCCA ACGTGTCTTG TAAGGTGCGG CTAGAAACTG      60
GGGAC ATG GCA GCG CCT GGC CCA GCG CTC TGC CTC TTC GAC GTG GAT GGG      110
Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly
      -15                      -10                      -5

AGG CTC ACC GCG CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC      158
Thr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe
      1                      5                      10

CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG      206
Leu Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser
      15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 159..278
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 107..160
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 166..250
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 114..167
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 148..201
id R09724
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..54
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..51
id R09724
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 101..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 200..229
id R09724
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 101..178
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 170..247
id W90369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..103
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 121..171
id W90369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 173..218
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 240..285
id W90369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..103
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..90
id N56221
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 126..182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACTT   60
GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC   120
GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC   170
    Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
          -15                      -10                      -5

GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG   218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
          1                      5                      10

ACA CTG   224
Thr Leu

```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..216
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 235..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..303
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 107..310
id T80259
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 15..114
id T80259
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..245
id T31768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 271..327
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 234..290
id T31768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..327
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 47..272
id N32697
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..97
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..43
id N32697
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..327
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..263
id N44613
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GCCTAGGTGT TSTCGTCCCT GCTAGTACTC CGGGCTGTGG GGGTCGGTGC GGATATTCAG 60
TCATGAAATC AGGGTAGGGA CTTCTCCCGC AGCGACGCGG CTGGCAAGAC TGTTTGTGTT 120
GCGGGGGCCG GACTTCAAGG TGATTTTACA ACGAG ATG CTG CTC TCC ATA GGG 173
                               Met Leu Leu Ser Ile Gly
                               -10

ATG CTC ATG CTG TCA GCC ACA CAA GTC TAC ACC ATC TTG ACT GTC CAG 221
Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln
      -5                      1                      5

CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GYA GAC ATT TTA GCA 269
Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Xaa Asp Ile Leu Ala
  10                      15                      20                      25

TAT AAC TTT GAA AAT GCA TCT CAG ACA TTT GAT GAC CTC CCT GCA AGA 317
Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Arg
                      30                      35                      40

TTT GGT TAT 326
Phe Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..368
id AA150637
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 30..294
id H02768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..372
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..339
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..147
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(267..394)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 231..358
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(184..277)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 349..442
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(109..164)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 464..519
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 72..250
id N30922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..180
(C) IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

AATCGCGGAG TCGGTGCTTT AGTACGCCGC TGGCACCTTT ACTCTCGCCG GCCGCGCGAA      60
CCCGTTTGAG CTCGGTATCC TAGTGCACAC GCCTTGCAAG CGACGGCGCC ATG AGT      116
                                         Met Ser
                                         -25

CTG ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC      164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
          -20                      -15                      -10

ATT GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT      212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
          -5                      1                      5

TAT GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG      260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
          10                      15                      20                      25

AAA GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTS RNA      308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Xaa Xaa
          30                      35                      40

GAT AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC      356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
          45                      50                      55

TGT GAT GGG GCT CAC ACA ARM VAT AAC GAA GAG ACT GGG CTG      398
Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
          60                      65                      70

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..150
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 31..126
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 151..212
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 126..187
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..35
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 211..242
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..216
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..263
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 202..410
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 172..206
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 159..280
id R54574

(B) LOCATION: 174..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 279..340
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 129..163
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 189..299
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 298..338
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 159..193
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 337..371
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..252
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTTCATC TTCTTGTTT CATCYTAAAT    60
ACCAACSTC ATG TCT GGT TCT AAT GGT TCC AAA GAA AAT TCT CAC AAT AAG    111
    Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys
        -60                -55                -50

GGT CGG ACG TCT CCT TAC CCA GGT TCA AAA GTT GAA CGA AGC CAG GTT    159
Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
        -45                -40                -35

CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG TGG CAA GAC TAT AAG CCT    207
Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
        -30                -25                -20

GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT GGA CCC AGG TGG GCA GAT    255
Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
        -15                -10                -5                1

CCT CAG ATC AGT GAV AGT VAT TTT TCT CCC AAG TTT AAC GAA AAG GAT    303
Pro Gln Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp
        5                10                15

GGG CAT GTT GAG ASA NAG AGC AAG AAT GGC CTG TAT GAG ATT GAN AAT    351
Gly His Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn
        20                25                30

GGA AGA CCG AGA AAT CCT GCA GAC GGA CTG GAC TGG TGG GCC    393
Gly Arg Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
        35                40                45

```

(2) INFORMATION FOR SEQ ID NO: 269:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(vii) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 137..335
id HSC1QH021
est

(viii) FEATURE:

region 126..263
id HUML12288
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..87
id HUML12288
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..266
id R60742
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 133..232
id HSC07D011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 35..129
id HSC07D011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..32
id HSC07D011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 136..230
id C04685
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..147

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 10..132
 id C04685
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 349..438
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AAAACCTTAG CAAGATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA   60
ATGSSCGTAT CAGGGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA  120
AGAAGAAAAG GACAATAMTC CARPTYCCTG GMCCVAASTA TTTCTACGAT GTGGAGGCTC  180
TSAGSSATTA CTTGCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAAT CGATCTTACA  240
CCTGGCTGGA GAAGCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG  300
GAGGCGCAGT CAAGTTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT   357
                                   Met Ala Ile
                                   -30

TCT CTC AGG AGT TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG   405
Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp
      -25                      -20                      -15

ATG CGG TGG ACT GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA   453
Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile Xaa Ala Glu
      -10                      -5                      1                      5

CCT CCG CAG CTG GAC ATC TCG                                         474
Pro Pro Gln Leu Asp Ile Ser
                        10
  
```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (B) TISSUE TYPE: HEART

[illegible]

(1X) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..51
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..97
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FVLGSA RLGGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

AACATTAACC	GGCAGG	ATG TCG GAG GTG CGG CTG CCA CCG CTA CGC GCC CTG	52
		Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu	
	-25	-20	
GAC GAC TTT GTT CTG GGG TCG GCG CGT CTT GGC GGC TCC GGA TCC ATG			100
Asp Asp Phe Val Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met			
-15	-10	-5	1
CGA CCC GCT GCG ATG GTG YHA CCG CGT CAT CAA CAA CCT CCT CTA CTA			148
Arg Pro Ala Ala Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu			
	5	10	15
CCA AAC CAA CTA CCT TCT CTG CTT CGG CAT CGG CCT CGC TCT CGC CGG			196
Pro Asn Gln Leu Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg			
	20	25	30
GTA CGT ACG GCC ACG			211
Val Arg Thr Ala Thr			
	35		

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 177..257
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 107..177
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 52..102
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 132..174
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id N44655
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..170
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..226
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..40
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 63..169
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 169..249
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..39
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 206..250
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGGCGGCGAA GATGCGGGAG AACACGGGTC GCGCCGGCAA GAGCAGCGGG AGCGNCGCGN 60
GGAAGGGGGC GSTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC 120
AGCGAGGCCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG 180
TGAATCGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG 232
                Met Lys Leu Val Ser Ala Thr Ala Trp
                -15                               -10
TTC GAG GAR TGC TGG TGG AGC GAA CTG TCA 262
Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 272:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(12) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(13) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 142..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 120..360
id HUML1108
est

(13) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..127
id HUML1108
est

(13) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..395
- (C) IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 137..500
id HSU51712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 112..270
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 9..111
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 105..213
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 206..315
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 314..347
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 309..410
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.3
seq LYVPLLAVCCLES/...

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

AASCTTCCAA ACCCAGGGCT TGCCTTGCC TTTGCCTCTT CCACCGCGCA GGGACCATGT    60
CGGCGGAGAG CGCGAGCGGC CCCACAGAGG ACCAGGTGGA AATCCTGGAG TACAACTTCA    120
ACAAGSTCGA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC    180
TTTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG    240
AAGGCTTCCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC    300
TTCACTCC ATG AAG GGC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG    350
Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu
      -30                      -25

TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GCT GTC TGC    398
Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys
-20          -15          -10          -5

TGT TTA CAC AGT GTT GTA TTT TTT    422
Cys Leu His Ser Val Val Phe Phe
      1

```

(2) INFORMATION FOR SEQ ID NO: 273:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: cDNA

(111) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(112) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 179..401
to AA010386
est

(113) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

(A) NAME/KEY: other
(B) LOCATION: 108..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 91..188
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 443..505
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 429..491
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..449
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 402..434
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..187
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..494
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 300..473
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 195..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 178..313
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..513
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..445
id W44481
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..193
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 184..289
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 340..396
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 291..342
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 397..440
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..289
id W40172
est

ix) FEATURE:

- (A) NAME/KEY: other

id W40172
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 85..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LMIALTVVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

ACTCCAACGC	TGGGTGACAT	TGAGCTCACC	AGCGCCACCG	TCCCCGGCGA	AGTTCTGCGC	60
TGGTCTGGCGG	AGTAGCAAGT	GGCC	ATG GGG AGC CTC AGC GGT CTG CGC CTG		111	
			Met Gly Ser Leu Ser Gly Leu Arg Leu			
			-115	-110		
GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT	159					
Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser						
	-105	-100	-95			
CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC	207					
Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys						
	-90	-85	-80			
ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA	255					
Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg						
	-75	-70	-65			
GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATC CTC ATA TGG	303					
Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp						
	-60	-55	-50			
TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT CTC TCG TTG	351					
Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu						
	-45	-40	-35	-30		
GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT	399					
Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr						
	-25	-20	-15			
CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG	447					
Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu						
	-10	-5	1			
GGC AAG AAG GCT GCC CAA AGA CAC GAG ACT TTA ACA AGC TTG MAC TTA	495					
Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu						
	5	10	15			
GAA AAG AAA GCT CGT CTG	513					

Glu Lys Lys Ala Arg Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 190..399
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..141
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 139..198
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 139..341
id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other

id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 144..300
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..95
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 93..152
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 122..338
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..73
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 71..130
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..360
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 121..283
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..72
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 346..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 270..326
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 70..129
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..358
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGGLG/PI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

ACTGTTTNGG GGAGGCGCGT GGGGCTTGAG GCCGAGAACG GCGCTTGCTG CCACCAAC      58
ATG GAG ACT TTG TAC CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC      106
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100                      -95                      -90                      -85

ATG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCG GGC ATG ACT      154
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80                      -75                      -70

GTG TAT GCT CTG GTG GTG GTG TGT TAC TTC CTC ATT ACC GGA GGA ATA      202
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65                      -60                      -55

```


Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile
20 25 30
CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG 243
Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 276:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 77..206
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..77
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 59..194
id HUM427610P
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..66
id HUM427610P

(B) LOCATION: 112..241
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 52..181
 id R52722
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 62..113
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 1..52
 id R52722
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 111..241
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 79..209
 id W41484
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..137
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq NIESLAWTG GTLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAGTTTCCTG	CGAGCTCGGC	TTCCTCAAC	ATG	GCT	GCG	CCC	TTG	TCA	GTG	GAG	53
	Met	Ala	Ala	Pro	Leu	Ser	Val	Glu			
	-35								-30		
GTG GAG TTC	GGA GGT GGT	GCG GAS	TCC	TGT	TTG	ACG	GTA	TTA	AGA	AAC	101
Val Glu Phe	Gly Gly Gly	Ala Xaa	Ser	Cys	Leu	Thr	Val	Leu	Arg	Asn	
	-25		-20						-15		
ATC GAG TCA	CTT GCC TGG	ACA GGA	GGA	ACC	CTG	GGA	CAT	CCG	GAA	CCT	149
Ile Glu Ser	Leu Ala Trp	Thr Gly	Gly	Thr	Leu	Gly	His	Pro	Glu	Pro	
	-10		-5				1				
GCT CAT CTG	GAT CAA GAA	GAA TTT	GCT	AAA	AGA	GCG	GCC	ASA	GTT	GTT	197
Ala His Leu	Asp Gln Glu	Glu Phe	Ala	Lys	Arg	Ala	Ala	Xaa	Val	Val	
5		10		15			20				
CAT CCA GGG	AGA CAG CGT	GCG GCC	AGG	AAT	TCT	GGT	GCT	GAC	TAC	AGG	245
His Pro Gly	Arg Gln Arg	Ala Ala	Arg	Asn	Ser	Gly	Ala	Asp	Tyr	Arg	
	25		30					35			

(2) INFORMATION FOR SEQ ID NO: 277:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..382
id AA127626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 44..329
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 330..384
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..60
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..39
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 68..424
id N32838
est

(ix) FEATURE:

- (A) NAME/KEY: other

id AA121528
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 130..344
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 36..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..130
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..392
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTCGCTGCT    60
TTTTAAGTTT CAAATTGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA   120
TCTTCACAGC ACAGTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTTGAA TAACTGGGAG   180
ATGAAACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA       230
      Met Thr His Leu Ile Glu Tyr Asp Arg His Arg
      -65                      -60                      -55

AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT       278
Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp
      -50                      -45                      -40

CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG       326
His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro
      -35                      -30                      -25

CCC ACT GTG GAC TCT GAG GCC TCT GCA TTT GTG GGT GGT CTG CCT GTG       374
Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val
      -20                      -15                      -10

ATA TTT TGG TCA TGG GCT GGT CTG GTC                                   401
Ile Phe Trp Ser Trp Ala Gly Leu Val
      -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..268
id HSC2SG081
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..181
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 184..262
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..230
id H0ML13589
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..136
id H05577
est

(D) OTHER INFORMATION: identity 100
region 139..220
id H05572
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```
AACAGTTACG CGCCGCACGG ATC ATG GCC GCA GCC GCT CTG GGG CAG ATC TGG      53
                   Met Ala Ala Ala Ala Leu Gly Gln Ile Trp
                   -20                               -15

GCA CGA AAG CTT CTC TCT GTC CCT TGG CTT CTG TGT GGT CCC AGA AGA      101
Ala Arg Lys Leu Leu Ser Val Pro Trp Leu Leu Cys Gly Pro Arg Arg
-10                               -5                               1

TAT GCC TCC TCC AGT TTC AAG GCT GCA GAC CTG CAG CTG GAA ATG ACA      149
Tyr Ala Ser Ser Ser Phe Lys Ala Ala Asp Leu Gln Leu Glu Met Thr
  5                               10                               15                               20

CAG AAG CCT CAT AAG AAG CCT GGC CCC GGC GAG CCC CTG GTG TTT GGG      197
Gln Lys Pro His Lys Lys Pro Gly Pro Gly Glu Pro Leu Val Phe Gly
                25                               30                               35

AAG ACA TTT ACC GAC CAC ATG CTG ATG GTG GAA TGG AAT GAC AAG GGC      245
Lys Thr Phe Thr Asp His Met Leu Met Val Glu Trp Asn Asp Lys Gly
                40                               45                               50

TGG GGC CAG CCC CGA ATC CAG CCC TTC CAG AAC CTC ACG CTG CAC CCA      293
Trp Gly Gln Pro Arg Ile Gln Pro Phe Gln Asn Leu Thr Leu His Pro
                55                               60                               65

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC      335
Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly
  70                               75                               80
```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 50..169
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 213..338
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 2..336
id W79731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..326
id H21245
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 34..305
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 302..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 306..348
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 41..202
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 201..284
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..266
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 283..344
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 266..327
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

AAGGGGTCGG AGGTCAGGGC GAGCGTCTCG CAGGCCGTAG GAGGAAG ATG GCG GTG	56
Met Ala Val	
GAG TCG CGC GTT ACC CAG GAG GAA ATT AAG AAG GAG CCA GAG AAA CCG	104
Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro Glu Lys Pro	
-35 -30 -25 -20	
ATC GAC CGC GAG AAG ACA TGC CCA CTG TTG CTA CTG GTC TTC ACC ACC	152
Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val Phe Thr Thr	
-15 -10 -5	
AAT AAC GGC CGC CAC CAC CGA ATG GAC GAG TTC TCC CGG GGA AAT GTA	200
Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg Gly Asn Val	
1 5 10	
CCG TCC AGC GAG TTG CAG ATC TAC ACT TGG ATG GAT GCA ACT TTG AAA	248
Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala Thr Leu Lys	
15 20 25	
GAA CTG ACA AGC TTA GTA AAA GAA GTC TAC CCA GAA GCT AGA WAG AAG	296
Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala Arg Xaa Lys	
30 35 40 45	
GGC ACT CAC TTC AAT TTT GCA VTC GTT TTT ACA GAT GTT AAA AGA CCT	344
Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val Lys Arg Pro	
50 55 60	

(xii) INFORMATION FOR SEQ ID NO: 280:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 72..338
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 332..363
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..280
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 274..305
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 24..290
id H81957
est

region 59..324
id W82998
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 64..329
id AA023811
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 240..305
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ACTAGCCTGC GAGTGTCTTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA    60
GTAGTGAAAA CGTTGCTTCT GAGGGGTGTC CAAGATGASC GGTTCAMCG GAGKTCAAGC    120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCAGT    180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TCGTCTCTA CGATGTGCCG GCCAACTCC    239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC    287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
      -20                      -15                      -10

TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA    335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
      -5                      1                      5                      10

ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG    383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
              15                      20                      25

CCC CTA TCA GAT GTG TTG    401
Pro Leu Ser Asp Val Leu
      30
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 72..257
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 33..75
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..34
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 75..260
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..78
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 39..159
id R57601
est

(ix) FEATURE:

region 144..223
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..42
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 84..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 55..166
id W71083
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ATAGGCGCAA G ATG GCG CTG CTT TTT GCA CGT TCT TTG CGC TTG TGC CGC	50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg	
-85 -80 -75	
TGG GGA GCC AAA CGA TTG GGA GTT GCC TCC ACA GAG GCC CAG AGA GGC	98
Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly	
-70 -65 -60	
GTC AGT TTC AAA CTG GMA GAA AAA ACC GCC CAC AGC AGC CTG GCA CTC	146
Val Ser Phe Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu	
-55 -50 -45	
TTC AGA GAT GAT ACG GGT GTC AAA TAT GGC TTG GTG GGA TTG GAG CCC	194
Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro	
-40 -35 -30	
ACC AAG GTG GCC TTG AAT GTG GAG CGC TTC CGG GAG TGG GCA GTG GTG	242
Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val	
-25 -20 -15 -10	
CTG GCA GAC ACA GCG GTC ACC AGT GGC AGA GGG	275
Leu Ala Asp Thr Ala Val Thr Ser Gly Arg Gly	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE.
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 77..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

ATTCCCCCTT GGSCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GCGGCAGCA    60
ACAGCGACTA CGAGGGG ATG GCG GCG GCT GCA GCA GGA ACT SNA ACA TCC CAG    112
          Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln
                    -65                                -60

AGG TTT TTC CAG AGC TTC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG    160
Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln
    -55                                -50                                -45

GCG GCG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT    208
Ala Ala Leu Glu Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp
    -40                                -35                                -30                                -25

GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT    256
Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn
          -20                                -15                                -10

TAC TGT GTT GCT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA    304
Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro
          -5                                1                                5

AAT AAT TCC ACT GCT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA    352
Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu
    10                                15                                20

AAA AAG TAT GGT GGT GCC CTA GAA ACT TTT TAC AGA AGG ACG GGG    397
Lys Asn Tyr Ala Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
    25                                30                                35

```

SEE INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 79..380
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..55
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 82..363
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..58
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..337
id R52491
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 65..247
id R21494
est

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..53
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..52
 id R21494
 est

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 266..305
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 268..307
 id R21494
 est

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 129..321
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 71..263
 id AA084554
 est

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 315..379
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 256..320
 id AA084554
 est

(1x) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 139..318
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq WFYIGSSLNGTRG/KR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AGTGGCTGCG ATGTTGCGTG CAGTTGCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA   60
CTTTCAATTA TGGCATGGCT GTGATATTC AACCAGCATG CTTTGGACTT TATTSYGSGA   120
AGAGCTATT ATTTAAAA ATG GCT CAA CTG AAA TAT ATG GAG AAT GTG GGG   171
      Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly
      -60              -55              -50

TAT GCT CAA GAG GAC AGA GGA CGA ATG CAC AGA AAT ATT GTC AGC CTT   219
Tyr Ala Gln Gln Asp Arg Gln Arg Met His Arg Asn Ile Val Ser Leu
      -45              -40              -35

```

CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG	315
Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg	
-15 -10 -5	
GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG	363
Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu	
1 5 10 15	
AAT GCA GCA TGG CCG CGG	381
Asn Ala Ala Trp Pro Arg	
20	

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..292
id HUM524F05B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 48..176
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..279
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..43
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 16..50
id H81799
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..181
id T84779
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 175..234
id T84779
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..45
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..51
id T84779
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 101..228
id W81213
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..107
id W81213
est

(1x) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..165
id AA030080
est

- (C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..202
id AA090080
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 174..266
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq WSPLSTRSGGTHA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
AAAAACAATA GGACGGAAAC GCCGAGGAAC CCGGCTGAGG CGGCAGAGCA TCCTGGCCAG   60
AACAAGCCAA GGAGCCAAGA CGAGAGGGAC ACACGGACAA ACAACAGACA GAAGACGTAC  120
TGSCCSCTGG ACTCCKCTGC CTCCCCATC TCCCCGCCAT CTGCGCCCGG AGG ATG   176
                                     Met
AGC CCA GCC TTC AGG GCC ATG GAT GTG GAG CCC CGC GCC AAA GGS TCC   224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                -25                -20                -15

TTC TGG AGC CCT TTG TCC ACC AGG TCG GGG GGC ACT CAT GCG TGC TCC   272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
      -10                -5                1

GCT TCA ATG AGA CAA CCC TGG   293
Ala Ser Met Arg Gln Pro Trp
      5
```

(xii) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 26..326
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 42..342
id R71425
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 11..337
id AA133412
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..345)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 172..403
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(71..114)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 402..445
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(26..76)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 439..489
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 186..359
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..192
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..76
(C) IDENTIFICATION METHOD: blastn

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..307
id R81019
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 18..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SILAQVLDQSARA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AGCGCTGACG CCGAGCC ATG GCG GAC GAG GAG CTT GAG GCG CTG AGG AGA      50
      Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg
                        -50                                -45

CAG AGG CTG GCC GAG CTG CAG GCC AAA CAC GGG GAT CCT GGT GAT GCG      98
Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala
      -40                                -35                                -30

GCC CAA CAG GAA GCA AAG CAC AGG GAA GCA GAA ATG AGA AAC AGT ATC      146
Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile
      -25                                -20                                -15

TTA GCC CAA GTT CTG GAT CAG TCG GCC CGG GCC AGG TTA AGT AAC TTA      194
Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu
      -10                                -5                                1                                5

GCA CTT GTA AAG CCT GAA AAA ACT AAA GCA GTA GAG AAT TAC CTT ATA      242
Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile
      10                                15                                20

CAG ATG GCA AGA TAT GGA CAA CTA AGT GAG AAG GTA TCA GAA CAA GGT      290
Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly
      25                                30                                35

TTA ATA GAR ATC CTT AAA AAA GTA AGC CAA CAA ACA GAA AAG AHN ACA      338
Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr
      40                                45                                50

ACA GTG AGG
Thr Val Arg
      55

```

(x) INFORMATION FOR SEQ ID NO: 286:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 186..382

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 156..352
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 61..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 34..119
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 29..61

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 1..33
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 169..306
id H80945
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 30..122
id H80945
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 157..345

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5

```

AACAGCGGGC AGGGAAAGCC GCGGGAAGGG TACTCCAGGC GAGAGGCGGA CGCGAGTCGT   60
CSTGGGAGGA AAAGTGACTA GCTCCCCTTC GTTGTCAGCC AGGGACGAGA ACACAGCCAC   120
GCTCCDAMCC GGCTGCCHAA GRWTCCTTSG GCGGCG ATG TCG GCC GCC GGT GCC   174
                               Met Ser Ala Ala Gly Ala
                               -60
CGA GGC CTG CGG GCC ACC TAC CAC CGG CTC CTC GAT AAA GTG GAG CTG   222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55                               -50                               -45
ATG CTG CCC GAG AAA TTG AGG CCG TTG TAC AAC CAT CCA GCA GGT CCC   270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40                               -35                               -30
AGA ACA GTT TTC TTC TGG GCT CCA ATT ATG AAA TGG GGG TTG GTG TGT   318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25                               -20                               -15                               -10
GCT GGA TTG GCT GAT ATG GCC AGA CCT GCA GAA AAA CTT AGC ACA GCT   366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5                               1                               5
CAA TCT GVK GTT TTG ATG GCT ACA GGG TTT ATT TGG TCA AGA TAC TCG   414
Gln Ser Xaa Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10                               15                               20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 185..380
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..192
id W07314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..478
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 401..470
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..390
id W07582
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..393
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..379
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..37
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..375
id AA112776
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..326
id H72671
est

(ix) FEATURE:

seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

```

AACTTGTCAG CCCTTGCTCTG AGGCGGAGGC AGCCCCGCGC CGCGCCGGAC CCGAGCATAT   60
TTCATTTTCT GTCATTGGAC TTTGAGCCAT TAGAACC ATG AGC AAC TAC AGT GTG   115
                               Met Ser Asn Tyr Ser Val
                               -85
TCA CTG GTT GGC CCA GCT CCT TGG GGT TTC CGG CTG CAG GGC GGT AAG   163
Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg Leu Gln Gly Gly Lys
-80                               -75                               -65
GAT TTC AAC ATG CCT CTG ACA ATC TCT AGT CTA AAA GAT GGC GGC AAG   211
Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu Lys Asp Gly Gly Lys
                               -60                               -55                               -50
GCA GCC CAG GCA AAT GTA AGA ATA GGC GAT GTG GTT CTC AGC ATT GAT   259
Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val Val Leu Ser Ile Asp
                               -45                               -40                               -35
GGA ATA AAT GCA CAA GGA ATG ACT CAT CTT GAA GCC CAG AAT AAG ATT   307
Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu Ala Gln Asn Lys Ile
                               -30                               -25                               -20
AAG GGT TGT ACA GGA NYT TTG AAT ATG ACT CTG CAA AGA GCA TCT GCT   355
Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr Leu Gln Arg Ala Ser Ala
-15                               -10                               -5
GCA CCC AAG CCT GAG CCG GTT CCT GTT CAA AAG CCC ACA GTC ACC AGC   403
Ala Pro Lys Pro Glu Pro Val Pro Val Gln Lys Pro Thr Val Thr Ser
 1                               5                               10                               15
GTG TGT TCC GAG ACT TCT CAG GAG CTA GCA GAG GGA CAG AGA AGA GGA   451
Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln Arg Arg Gly
                20                               25                               30
TCC CAG GGT GAC AGT AAA CAG CAA AAT                               478
Ser Gln Gly Asp Ser Lys Gln Gln Asn
        35                               40

```

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 4..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..330
id N35568
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..297
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..272
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 295..338
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 271..314
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..212
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 209..313
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 13..320
id HSC1MA011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 245..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEAIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

ATTCGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATCCCA   60
ACGGATTTGA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT  120
TTTTGAACAA GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC  180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCCAG  240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG   289
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
      -15                -10                -5

GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CTG CAG GCC   337
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
      1                5                10

TCG AAG GAG CTC CAG CAA
Ser Lys Glu Leu Gln Gln
      15

```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 90..178
id W21198
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 2..53
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..89
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 269..345
id AA058174
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 204..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALLCTLLLHFQNI/RR

ii. SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGTTTCTTGGATCGGAGG GAGGTTCCGG TGGGCATCGG GCGGCTGGAA GAGCTCGACT 60
CGTCCGCTTCTTGGAAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTTGCAG AGCGGCTGTC 120
TAACTTCTTCTTGGACTACTG GAAGTCACAG CCAAAGAAAT TCTGTGATTA CTGCAAGTGC 180
TAACTTCTTCTTGGACTACTG TCT ATG ATA ATT GCG GCG TTA GAG ATT TAA TAA

Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr	
-30 -25 -20 -15	
AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA	329
Lys Ala Leu Leu Cys Thr Leu Leu Leu His Phe Gln Asn Ile Arg Arg	
-10 -5 1	
TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT	377
Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe	
5 10 15	
CAT CAA CCT GAC TTT GAT TAT ATA	401
His Gln Pro Asp Phe Asp Tyr Ile	
20 25	

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97
region 4..337
id HUMGPCRB
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..54
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 55..92
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..235

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4
seq LVFIIGLVGNLLA/LV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AACTTCAGTT TGSACAACTA CTCACAGCTA CTACACAGAG ACCCGAACGA GTCAGTGATA    60
TACACCTGGA CCACACCA ATG GAT ATA CAA ATG GCA AAC AAT TTT ACT CCG    112
      Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro
      -50                                -45

CCG TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC TAT GCA CAT CAC    160
Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His
-40                                -35                                -30

AGC ACG GCG AGG ATA GTA ATG CCT CTG CAT TAC AGC CTC GTC TTC ATC    208
Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser Leu Val Phe Ile
-25                                -20                                -15                                -10

ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC ATT GTT CAA AAC    256
Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn
      -5                                1                                5

AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA AAT TTG GTT ATT    304
Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile
      10                                15                                20

TCT GAT ATA CTT TTT ACC ACC GCT TTG CCT ACA CGA ATA GCT ACT ATG    352
Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met
      25                                30                                35

CMA TGG GCG TTG ACT GGA GAA TCG GAG ATG TGG    385
Xaa Trp Ala Leu Thr Gly Glu Ser Glu Met Trp
      40                                45                                50

```

(2) INFORMATION FOR SEQ ID NO: 291:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: CDNA

(3) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Pancreas

(4) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..462
- (C) IDENTIFICATION METHOD: other

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..218
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 216..365
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 412..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 366..416
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..409
id C16991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 212..411
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 52..214
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..58

id N28784
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..303
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 303..408
id C17735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 47..209
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 263..406
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 207..350
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 406..462
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..407
id AA057588
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..53
id AA057588
est

(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG    60
CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG    120
GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT    180
TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CAGTGTGCAC    240
CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT    300
GWTTGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG    359
                                         Met

CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG    407
Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser
      -25                      -20                      -15

ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG    455
Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln
      -10                      -5                      1

CAG AGA
Gln Arg
5
                                         461

```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15
seq LFLLLLLAASAWG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln
-35                      -30                      -25                      -20

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Ala Ala Ser
      -15                      -10                      -5

```

Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser
 1 5 10
 Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
 15 20 25
 Tyr Leu Pro Ala Thr
 30

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.2
seq LLLXAVLLSLASA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Xaa Ala Val Leu Leu
 -20 -15 -10
 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 -5 1 5 10
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 15 20 25
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 30 35 40
 Glu Ser Glu Leu Glu Xaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
 45 50 55
 Ser Lys Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser
 60 65 70 75

(2) INFORMATION FOR SEQ ID NO: 294:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.1

seq CVLLLLLLLLLTRS/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
-20 -15 -10

Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln
-5 1 5 10

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
15 20 25

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
30 35 40

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
45 50 55

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
60 65 70 75

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
80 85 90

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu
95 100

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLFLFLAVDEAWA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val
-20 -15 -10

Asp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 296: -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
seq SLLLAVALGLATA/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Lys Ser Leu Ser Leu Leu Leu Ala Val Ala Leu Gly Leu Ala Thr
-15 -10 -5

Ala Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp
1 5 10 15

Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg
20 25 30

Gln Gly Pro Gly Ala Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu
35 40 45

Ile Leu Ser Val His Asp Pro Ala Gly Ala Leu Gln Ala Arg
50 55 60

INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.6
seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala
-15 -10 -5

Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu
1 5 10 15

Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu
20 25 30

Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys
35 40 45

Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly
50 55 60

Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly
65 70 75 80

Met Val Met Tyr Thr Ser Lys Asp Arg
85

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.4
seq LIILIXIWIWCLG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln
-45                      -40                      -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr
-30                      -25                      -20                      -15

Ile Leu Ile Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
-10                      -5                      1

Thr Phe Gly Thr Ser Thr Thr Lys Ser Val Gln Leu Lys Ile Leu Arg
5                      10                      15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile
20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.4
seq LPFLLSLFPGALP/VQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val
-30                      -25                      -20                      -15

Leu Leu Pro Phe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln
-10                      -5                      1

Ile Arg Tyr Ser Ile Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly
5                      10                      15

Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg
20                      25                      30

Lys Leu Arg Val Ser Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu
35                      40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq IIFLCHLLRGLHA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly
 -30 -25 -20

Ala Lys Thr Phe Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His
 -15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln
 1 5 10 15

Thr His Gly Arg Leu Pro
 20

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -104..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LTSLSWLLXASCS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys Ala Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

```

                -100                -95                -90
Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
      -85                -80                -75
Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val
      -70                -65                -60
Leu Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
      -55                -50                -45
Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
      -40                -35                -30                -25
Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser
      -20                -15                -10
Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
      -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LATKLLSLSGVFA/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
      -70                -65                -60
Arg Thr Ser Val Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
      -55                -50                -45
Ala Thr Pro Ser Ala Arg Ala Ala Ala Val Val Ala Ala Ala Ala
      -40                -35                -30
Arg Thr Ser Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
      -25                -20                -15                -10

```

10 15 20

Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa
 25 30 35

Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu
 40 45 50 55

Val Val Gly Ile Gly Ala
 60

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VLWLISFFTFDGD/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
 -15 -10 -5

Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
 1 5 10 15

Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met
 20 25

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq WIFLAAILKGVQC/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
      -15                      -10                      -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
      1                      5                      10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
      15                      20                      25

Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      30                      35                      40                      45

Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly
      50                      55                      60

Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser
      65                      70                      75

Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln
      80                      85                      90

Ala Ile Tyr Tyr Cys Ala Thr
      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LWRLLLWAGTAFQ/VX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala
-20                      -15                      -10

Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala
-5                      1                      5                      10

Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr
15                      20                      25

Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr
30                      35                      40

Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn
45                      50                      55

Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala
60                      65                      70                      75

Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp
80                      85                      90

Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met
95                      100                      105

Thr Val Leu Leu Ser His
110

```

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu
-25                      -20                      -15                      -10

Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro
-5                      1                      5

Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly
15                      20

```



```

Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln
 25                      30                      35

Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro
 40                      45                      50                      55

Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp
        60                      65                      70

Leu Val Arg Pro Ser Pro Leu Thr Pro
      75                      80

```

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LCFLLLAVAMSFF/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
      -20                      -15                      -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
      -5                      1                      5

Thr Arg Ala His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly
      10                      15                      20

Ser Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
      25                      30                      35                      40

Thr Leu Val Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
      45                      50                      55

Pro Leu Val Ser Met His Phe Phe
      60

```

(A) LENGTH: 128 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LVLVLVVAVTVRA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg
-15 -10 -5
Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val
1 5 10 15
Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu
20 25 30
Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His
35 40 45
Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala
50 55 60
Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr
65 70 75
Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu
80 85 90 95
Leu Leu Glu Leu Asp Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -102..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq LXMTLMLPFKILS/DS

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Thr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys
-100 -95 -90
Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg
-85 -80 -75
Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro
-70 -65 -60 -55
Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
-50 -45 -40
Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
-35 -30 -25
Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu
-20 -15 -10
Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
-5 1 5 10
Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
15 20 25
Val Gly Glu Gly
30

(2) INFORMATION FOR SEQ ID NO: 310:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(12) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Spleen

(13) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -46..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq SIGVLTLSHLISG/LR

-45

-40

-35

Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly
 -30 -25 -20 -15

Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg
 -10 -5 1

Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LIILGLVLFMVYGV/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly
 -50 -45 -40 -35

Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val
 -30 -25 -20

Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val
 -15 -10 -5

Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu
 1 5 10

Arg Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser
 15 20 25 30

Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp
 35 40 45

Ala Ile Met Gln Met Trp Leu Asn Ala
 50 55

(1) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SCLVSGWGLLANG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
      -60                      -55                      -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
      -45                      -40                      -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
      -30                      -25                      -20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
      -15                      -10                      -5

Gln Arg
  1

```

2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq MLCGWEFLNLSL...

```

Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
  -45                      -40                      -35

Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
  -30                      -25                      -20

Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
-15                      -10                      -5                      1

Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
                      5                      10                      15

Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
  20                      25                      30

Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
  35                      40                      45

Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
  50                      55                      60                      65

Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa
                      70                      75                      80

Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln
                      85                      90                      95

```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLLFLAWVCFLFY/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu
  -15                      -10                      -5

Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg
  1                      5                      10

Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly
  15                      20                      25                      30

```

```

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala
      35                      40                      45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe
      50                      55                      60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val
      65                      70                      75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu
      80                      85                      90

Ile Gln Pro His His Ala Arg Leu
      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq CWMMLLGSGSFL/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly
-20                      -75                      -70

Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu
-65                      -60                      -55                      -50

Ile Gln Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala
      -45                      -40                      -35

Ala Ala Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe
      -30                      -25                      -20

Gly Cys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe
      -15                      -10                      -5

Ala Arg Met Thr Cys Xaa Trp Arg Ser
      -1

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq ILRLLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
-35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
-20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
15 20 25

Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly
30 35 40

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLRVNLNLPNSIG/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:


```

Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro
-20                      -15                      -10

His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu
-5                      1                      5                      10

Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa
15                      20                      25

Asn Ser Cys Thr Ala Leu Gln His Leu Asp
30                      35

```

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq ILRLLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
-35                      -30                      -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
-20                      -15                      -10                      -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
1                      5                      10

Leu Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
15                      20                      25

Arg

```

INFORMATION FOR SEQ ID NO: 319:

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Colon
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -13..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq MVLLTMIARVADG/LP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
    -10                      -5                      1
Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
    5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -47..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq GCGMFTFLSSVXA/AV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
    -45                      -40                      -35
Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
    -30                      -25                      -20
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala
    -15                      -10                      -5                      1
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
    5                      10                      15
Leu Leu Gln Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Gln Glu

```

20

25

30

Met Val Val Ser Ser Leu Val Ile Gly .
35 40

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LLFPVGRSWSCFA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val
-20 -15 -10

Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr
-5 1 5

Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser
10 15 20

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp
-15          -10          -5          1
Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala
          5          10          15
Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu
          20          25          30
Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr
          35          40          45
Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr
          50          55          60          65
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
          70          75          80
Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr
          85          90          95

```

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLLSDILGQGATA/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```

Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
-20          -15          -10
Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
-5          1          5          10
Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
          15          20          25
Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
          30          35          40

```

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly
45 50 55

(1) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (E) TYPE: AMINO ACID
- (F) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (E) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (F) OTHER INFORMATION: score 4.9
seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr
1 5 10 15

Tyr Cys Leu Thr Thr Pro Gln
20

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (E) TYPE: AMINO ACID
- (F) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (E) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (F) OTHER INFORMATION: score 4.9

```

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
      -40                      -35 .                      -30

Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu
      -25                      -20                      -15

Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg
      -10                      -5                      1                      5

Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile
              10                      15                      20

Gln Trp Ile Xaa Lys Gln Xaa Gly Met
      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq QLLLATLQEAATT/QE

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
-70                      -65                      -60                      -55

Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
      -50                      -45                      -40

Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
      -35                      -30                      -25

Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
      -20                      -15                      -10

Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
      -5                      1                      5                      10

Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
              15                      20                      25

Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
              30                      35                      40

```

Gln Leu Ser Pro Ser
45

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLPFGMLCASSTT/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

```

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro
-25                -20                -15

Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His
-10                -5                1                5

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
10                15                20

Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
25                30                35

Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
40                45                50

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu
55                60                65

```

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -110..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq HTXGLLGFRXQG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110                -105                -100                -95

Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
                -90                -85                -80

Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
                -75                -70                -65

Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
                -60                -55                -50

Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
-45                -40                -35

Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30                -25                -20                -15

Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
                -10                -5                1

Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa
        5                10                15

Thr Trp Arg Glu Thr Trp
        20

```

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Large intestine

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq PLSMILLSDKIQS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:


```

Met Lys Val Thr Gly Ile Thr Ile Leu Phe Trp Pro Leu Ser Met Ile
      -20              -15              -10

Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys Arg Glu Val Gln Cys Asn
      -5              1              5

Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro Ala Asp Ile Lys Lys Asp
      10              15              20

Val Thr Ile Leu Asp Leu Ser Tyr Asn Gln Xaa Thr Leu Asn Gly Thr
      25              30              35              40

Asp Thr

```

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq HLSWSSSAYQAWA/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Ala Ala Gly Arg Ala Gln Val Pro Ser Ser Glu Gln Ala Trp Leu
      -95              -90              -85

Glu Asp Ala Gln Val Phe Ile Gln Lys Thr Leu Cys Pro Ala Val Lys
      -80              -75              -70              -65

Glu Pro Asn Val Gln Leu Thr Pro Leu Val Ile Asp Cys Val Lys Thr
      -60              -55              -50

Leu Trp Leu Ser Gln Gly Arg Asn Gln Gly Ser Thr Leu Pro Leu Ser
      -45              -40              -35

Tyr Ser Phe Val Ser Val Gln Asp Leu Lys Thr His Gln Arg Leu Pro
      -30              -25              -20

Leu Thr Ser His Leu Ser Trp Ser Ser Ser Ala Thr Gln Ala Thr Ala

```

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq STCCWCTPGGAST/ID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Ser Thr Cys Cys Trp Cys Thr Pro Gly Gly Ala Ser Thr Ile Asp
 -10 -5 1
Phe Leu Lys Arg Tyr Ala Ser Asn Thr Pro Ser Gly Glu Phe Gln Thr
 5 10 15
Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VVEILPYLPCLTA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

-35

-30

-25

Ser Asn Phe Cys Xaa Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
 -20 -15 -10 -5

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
 1 5 10

Ser Gly Asn Arg Ala
 15

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -107..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq IVLVLLGGRYTEE/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys
 -105 -100 -95

Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu
 -90 -85 -80

Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln
 -75 -70 -65 -60

Leu Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 -55 -50 -45

Ile Gly Leu Phe Asp Thr Lys Glu Ser Leu Xaa Thr Thr Cys Lys Glu
 -40 -35 -30

Ile Xaa Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val
 -25 -20 -15

Leu Val Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LLXCVGNFFGSTQ/DA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Ala Gln Lys Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
          -45                      -40                      -35

Lys Phe Asp Ile Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser
          -30                      -25                      -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr
          -15                      -10                      -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro
  1              5              10              15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
          20              25              30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu
          35              40              45

Gly Arg Gly
          50

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -52...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Gln Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
   -50                      -45                      -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
   -35                      -30                      -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
  -20                      -15                      -10                      -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
                1                5                10

Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
   15                20                25

Ile Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His
   30                35                40

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile
   45                50                55
  
```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -52...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```

Met Gln Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Xaa Trp Lys Met
   -50                      -45                      -40
  
```

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 -20 -15 -10 -5
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 1 5 10
 Gln Gly

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser
 -35 -30 -25
 Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala
 -20 -15 -10 -5
 Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln
 1 5 10
 Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro
 15 20 25
 Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val
 30 35 40
 Glu Lys Asn Lys Tyr Asp Ala Thr Gly
 45 50

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -58..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVSFVSSSEGTEQ/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg
-55 -50 -45
Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp
-40 -35 -30
Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser
-25 -20 -15
Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser
-10 -5 1 5
Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg
10 15 20
Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys
25 30 35
Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro
40 45 50
Asn Ser Lys Gly Val Leu Met Phe Lys Lys Arg
55 60 65

(xii) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(iii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
   -35                      -30                      -25

Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
   -20                      -15                      -10

Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
   -5                      1                      5                      10

Leu His Glu Thr Gly Gly Ala Met Val Tyr
          15                      20

```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
          -25                      -20                      -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
          -10                      -5                      1

Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
          5                      10                      15

Asp Leu
    20

```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.6
seq LLALLTVSTPSWC/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu
-30 -25 -20

Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser Trp Cys
-15 -10 -5

Gln Ser Thr Glu Ala Ser Pro Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.8
seq SLLLLLLXCVHWS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Ala Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu
-25 -20 -15

Leu Leu Leu Leu Xaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser
-10 -5 1 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.2
                        seq AFLLLVALSYTLA/RD
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.3
 seq LVLLLVLTLLCSL/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala
-45                -40                -35

Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly
-30                -25                -20                -15

Ala Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
-10                -5                1

Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
5                10                15

Arg Gln Lys Ala Leu Ser Pro Lys
20                25
```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.1
 seq LLLQLAVLGAALA/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala
-15                -10                -5

Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr
1                5                10                15
```

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu
 50 55 60
 Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys
 65 70 75 80
 Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser
 85 90 95
 Lys Asp Gln Thr Ser Lys
 100

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.8
seq SALLVGFLSVIFA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala
 -25 -20 -15
 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
 -10 -5 1 5
 His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
 10 15 20
 Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile
 25 30 35
 Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
 40 45 50
 Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu
 55 60 65
 Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn
 70 75 80 85
 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala
 90 95 100

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LALSLILVLAFG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
-15 -10 -5

Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
1 5 10 15

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
20 25 30

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
35 40 45

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
50 55 60

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
65 70 75

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
80 85 90 95

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
100 105 110

311

(2) INFORMATION FOR SEQ ID NO: 348:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.4
seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1

Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15

Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30

His Pro Asp Asp Glu Ala Met Trp
35 40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8
seq LVFTVSLFAWICC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
-35 -30 -25

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
-20 -15 -10

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
-5 1 5 10

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro
 15 20 25

Glu Asn Leu Asn Ser Lys Lys Lys
 30

(ii) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
 -15 -10 -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
 1 5 10

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
 15 20 25 30

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
 35 40 45

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly
 50 55 60

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile
 65 70 75

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln
 80 85 90

Phe Arg Pro Ala Phe Ser Ala Ile Arg
 95 100

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq VLLTLLLI AFIFL/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met	Thr	Ala	Trp	Glu	Ala	Met	Ala	Pro	His	Val	Asn	Pro	Thr	Leu	Lys	
			-60					-55						-50		
Asp	Lys	Ala	Leu	Ser	Pro	Gln	Gln	Xaa	Xaa	Xaa	Thr	Ser	Pro	Ala	Pro	
		-45					-40					-35				
Cys	Xaa	Ser	Asn	His	His	Asn	Lys	Lys	His	Leu	Ile	Leu	Ala	Phe	Cys	
		-30				-25					-20					
Ala	Gly	Val	Leu	Leu	Thr	Leu	Leu	Leu	Ile	Ala	Phe	Ile	Phe	Leu	Ile	
	-15				-10				-5						1	
Ile	Lys	Ser	Tyr	Arg	Lys	Tyr	His	Ser	Lys	Pro	Gln	Ala	Pro	Gly		
			5					10					15			

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly
 -15 -10 -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
 1 5 10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile
 15 20 25 30

Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile
 35 40 45

Ser Glu

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LVXSLP VHCLTFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu
 -15 -10 -5

Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp
 1 5 10

Phe Xaa Ala Gln Ala His Xaa Pro Pro Leu Ile Leu Gly Pro
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15 -10 -5
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
1 5 10 15
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
20 25 30
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
35 40 45
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
50 55 60
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
65 70 75 80
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
85 90 95
Val Leu Ile Trp
100

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -59..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser
 -55 -50 -45

Ile His Arg Gln His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu
 -40 -35 -30

Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu
 -25 -20 -15

Ala Gln Leu Ala Phe Leu Ser Gln Ile Ser Gln Cys Ile Ile Ser Gln
 -10 -5 1 5

Arg

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFEVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 10 15 20

Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala
 25 30 35

Val Phe Leu Ile Ile Leu Phe Cys
 40

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu
-20 -15 -10
Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys
-5 1 5
Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly
10 15 20 25
Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile
30 35 40
Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu
45 50 55
Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -136..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys
-135                -130                -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe
-120                -115                -110                -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser
                -100                -95                -90

Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn
                -85                -80                -75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu
                -70                -65                -60

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu
-55                -50                -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn
-40                -35                -30                -25

Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro Leu Ile Ser Val Ala
                -20                -15                -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala
                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (E) OTHER INFORMATION: score 5.3
seq PLLKILHAAGAQQ/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala
                -40                -35                -30

```

-10

-5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln
 5 10 15 20

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq AFAWLGVVPLTAC/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly
 -110 -105 -100

Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile
 -95 -90 -85

Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg
 -80 -75 -70 -65

Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile
 -60 -55 -50

Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala
 -45 -40 -35

Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr
 -30 -25 -20

Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys
 -15 -10 -5

Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr
 1 5 10 15

Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu
 20 25 30

Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq MLIMLGIFNVHS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu
-10 -5 1

Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln
5 10 15

Asn Ile Tyr Asn Leu Tyr Glu His Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq AAVAVGMLXASYA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
 seq SDPLCVLFLNTSG/QQ
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Gln | Cys | Val | Thr | Lys | Val | Ala | Leu | Asn | Val | Ser | Cys | Ala |
|     |     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |
| Asn | Leu | Leu | Asp | Lys | Asp | Ile | Gly | Ser | Lys | Ser | Asp | Pro | Leu | Cys | Val |
|     |     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |
| Leu | Phe | Leu | Asn | Thr | Ser | Gly | Gln | Gln | Trp | Tyr | Glu | Val | Glu | Arg | Thr |
|     |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     |
| Glu | Arg | Ile | Lys | Asn | Cys | Leu | Asn | Pro | Gln | Phe | Ser | Lys | Thr | Phe | Ile |
| 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |
| Ile | Asp | Tyr | Tyr | Phe | Glu | Val | Val | Gln | Lys | Leu | Lys | Phe | Gly | Val | Tyr |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |



Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp Phe Leu Gly  
                   45                                  50                                          55

(C) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly  
 -70                                  -65                                          -60                                          -55

Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val  
                                   -50                                          -45                                          -40

Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser  
                                   -35                                          -30                                          -25

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe  
                                   -20                                          -15                                          -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys  
                                   -5                                          1                                          5                                          10

Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp  
                                   15                                          20                                          25

Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser  
                                   30                                          35

(C) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(1X) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.6  
seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys  
-25 -20 -15 -10

Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu  
-5 1 5

Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp  
10 15 20

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(3) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq MLAVSLTVXLLGA/MM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu  
-10 -5 1

Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro  
5 10 15

Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu  
20 25 30 35

Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile  
40 45 50

Gly Asp Val Met Phe Thr Gly Ser Trp  
                   55                  60

(2) INFORMATION FOR SEQ ID NO: 367:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
                                   seq MLELDLLVFHLWG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala  
   -75                  -70                  -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys  
   -60                  -55                  -50                  -45

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly  
                   -40                  -35                  -30

Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met  
                   -25                  -20                  -15

Leu Glu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys  
   -10                  -5                  1

Leu Val Thr Trp Gln Gly  
   5                  10

(2) INFORMATION FOR SEQ ID NO: 368:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -45..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13.9  
 seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45 -40 -35 -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
 -25 -20 -15

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
 -10 -5 1

Ser Arg Thr Asp Ser Pro Ser Pro Leu
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13.9  
 seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
-25 -20 -15 -10

Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
 -5 1 5

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
 10 15 20

Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6  
seq ILLCLLLALFASG/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
 -85 -80 -75

Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60

Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45

Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
 -40 -35 -30 -25

Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10

Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5

Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
 10 15 20

Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6  
seq VFCLLAAPGAHS/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly  
                    -15                    -10                    -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys  
                    1                            5                            10

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe  
          15                            20                            25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu  
          30                            35                            40                            45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala  
                    50                            55                            60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn  
                    65                            70                            75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val  
          80                            85                            90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu  
          95                            100                            105

Asp Ala Leu Asp Leu Trp  
110                            115

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg  
-110 -105 -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly  
-95 -90 -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly  
-80 -75 -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile  
-65 -60 -55 -50

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala  
-45 -40 -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys  
-30 -25 -20

Thr Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser  
-15 -10 -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met  
1 5 10 15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser  
20 25

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(x) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LMSLLLVLPWVEA/VE

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

-5

1

5

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp  
10 15 20

Gly Tyr Met His Gly  
25

## (2) INFORMATION FOR SEQ ID NO: 374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq ILVLMGLPLAQA/LD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro  
-20 -15 -10 -5

Leu Ala Gln Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn  
1 5 10

Cys

## (2) INFORMATION FOR SEQ ID NO: 375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11



seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
-15 -10 -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
1 5 10 15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
20 25 30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
35 40 45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
50 55 60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg
65 70 75 80

Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser
85 90 95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
100 105

```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq RLLLLPLLLAVSG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
-15 -10 -5

```

```

 15 20 25
Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
 30 35 40
Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Xaa Thr Arg
 45 50 55
Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln Glu Leu Gln Gly
 60 65 70 75
Gln Arg Ser Asp Val Tyr Ser
 80

```

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq LCRAICLFPRVFA/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 -20 -15 -10
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 -5 1 5
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
 10 15 20
Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys
 25 30 35 40
Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
 45 50 55
Gln Leu

```

## (2) INFORMATION FOR SEQ ID NO: 378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LMCLSLCTAFALS/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe  
                  -15                  -10                  -5

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro  
                  1                  5                  10

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp  
15                  20                  25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu  
30                  35                  40                  45

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile  
                  50                  55                  60

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys  
                  65                  70                  75

## (2) INFORMATION FOR SEQ ID NO: 379:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- A NAME/KEY: sig\_peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
-30 -25 -20 -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
 -10 -5 1

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 5 10 15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys
 20 25 30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val
 35 40 45 50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn
 55 60 65

Met Thr Cys

```

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
-20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
-5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Thr

```

45 50 55  
Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
60 65 70 75  
Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
80 85 90  
Gly Leu Ser Gly Lys Trp  
95

## (2) INFORMATION FOR SEQ ID NO: 381:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq LLWLALACSPVHT/XL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
-15 -10 -5  
Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(3) OTHER INFORMATION: score 9.3  
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
-15 -10 -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 1 5 10 15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa
 20 25 30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
-20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
-5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
 45 50 55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
60 65 70 75

```

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu  
80 85

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2  
seq LLXLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro  
-15 -10 -5  
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
1 5 10  
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
15 20 25  
Gly Leu Val Val Thr Asp Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```

Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40 -35 -30 -25

Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
 -20 -15 -10

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
 -5 1 5

Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
10 15 20

Cys Thr Gly Gly Met Glu
25 30

```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
 -10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
20 25 30 35

Val Lys Pro His Met
 40

```



## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq SAVLSGFVLGALA/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
 -15 -10 -5

Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
 1 5 10

Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser
 15 20 25

Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr
 30 35 40 45

Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
 50 55 60

Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val
 65 70 75

Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe
 80 85 90

Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln
 95 100 105

Asp Leu Val Phe Leu Leu Leu Thr Pro
 110 115

```

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20

Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15

Asp Pro Glu Arg
 20

```

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -136..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.7  
seq AVALSLFLGWLGA/DR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr
 -135 -130 -125

Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
 -120 -115 -110 -105

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 -100 -95 -90

```

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn  
-85 -80 -75  
Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val  
-70 -65 -60  
Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn  
-55 -50 -45  
Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser  
-40 -35 -30 -25  
Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser  
-20 -15 -10  
Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq LLWLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
-15 -10 -5  
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu  
-40 -35 -30  
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu  
-25 -20 -15  
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala  
-10 -5 1 5  
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr  
10 15 20  
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe  
25 30 35  
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser  
40 45

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.5  
seq LVLGLVLPLILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu  
-15 -10 -5  
Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile  
1 5 10

```

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp
 15 20 25 30
Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly
 35 40 45
Gln Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp
 50 55 60
Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu
 65 70 75
Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val
 80 85 90
His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn
 95 100 105 110
Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu
 115 120 125
Leu

```

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLTIVGLILPTRG/QT

## (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
-20 -15 -10
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
-5 1 5 10
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp

```

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly  
 45 50 55  
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg  
 60 65 70

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LALSSLLSLLLFA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg  
 -45 -40 -35  
 Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly  
 -30 -25 -20  
 Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly  
 -15 -10 -5 1  
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile  
 5 10 15  
 Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala  
 20 25 30  
 Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys  
 35 40 45  
 Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser  
 50 55 60 65  
 Gly Pro

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.3  
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln  
-35 -30 -25 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg  
-15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly  
1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly  
15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe  
30 35 40 45

Ile Glu Cys Glu Asp Arg  
50

(2) INFORMATION FOR SEQ ID NO: 396:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -53..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Val | Leu | Gly | Leu | Cys | Ser | Met | Ala | Ser | Trp | Ile | Pro | Cys |  |
|     |     |     | -50 |     |     |     |     | -45 |     |     |     |     | -40 |     |     |  |
| Leu | Cys | Gly | Ser | Ala | Pro | Cys | Leu | Leu | Cys | Arg | Cys | Cys | Pro | Ser | Gly |  |
|     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |     |  |
| Asn | Asn | Ser | Thr | Val | Thr | Arg | Leu | Ile | Tyr | Ala | Leu | Phe | Leu | Leu | Val |  |
|     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |  |
| Gly | Val | Cys | Val | Ala | Cys | Val | Met | Leu | Ile | Pro | Gly | Met | Glu | Glu | Gln |  |
| -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |  |
| Leu | Asn | Lys | Ile | Pro | Gly | Phe | Cys | Glu | Asn | Glu | Lys | Gly | Val | Val | Pro |  |
|     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |  |
| Cys | Asn | Ile | Leu | Val | Gly | Tyr | Lys | Ala | Val | Tyr | Arg | Leu | Cys | Phe | Gly |  |
|     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |  |
| Leu | Ala | Met | Xaa | Tyr | Leu | Leu | Leu | Ser | Leu | Leu | Met | Ile | Lys | Val | Lys |  |
|     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |  |
| Ser | Ser | Ser | Asp | Pro | Arg | Ala | Ala | Val | His | Asn | Gly | Phe |     |     |     |  |
| 60  |     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
                        seq IVRLVAFCPPFASS/QV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
-55 -50 -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val
-40 -35 -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
-25 -20 -15 -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
-5 1 5

Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu
 10 15 20
 Glu Thr His Leu Pro Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly
 25 30 35
 Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys
 40 45 50 55
 Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His
 60 65 70
 Phe His Asn Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys
 75 80 85
 His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met
 90 95

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser
 -45 -40 -35
 Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser
 -30 -25 -20
 Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
 -15 -10 -5 1
 Pro Pro Tar Gln Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly
 5 10 15

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
-25 -20 -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
-10 -5 1 5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly
10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FLLVRKLPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

[illegible]

(2) INFORMATION FOR SEQ ID NO: 401:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(2X) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
 seq FLLVRKLPPLCHG/LP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa Xaa Ala  
-65 -60 -55

Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val  
-50 -45 -40

Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu  
-35 -30 -25

Ileu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro  
-20 -15 -10

Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala  
30 35 40

Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg  
45 50 55

Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe  
60 65 70 75

Leu Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -48..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq LLMLLLFLSELOQ/YL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Ala | Leu | Gly | Lys | Leu | Lys | Gln | Phe | Asp | Ala | Tyr | Pro | Lys | Thr |  |
|     |     |     | -45 |     |     |     |     | -40 |     |     |     |     | -35 |     |     |  |
| Leu | Glu | Asp | Phe | Arg | Val | Lys | Thr | Cys | Gly | Gly | Ala | Thr | Val | Thr | Ile |  |
|     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |  |
| Val | Ser | Gly | Leu | Leu | Met | Leu | Leu | Leu | Phe | Leu | Ser | Glu | Leu | Gln | Tyr |  |
|     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |     |     |     |  |
| Tyr | Leu | Thr | Thr | Glu | Val | His | Pro | Glu | Leu | Tyr | Val | Asp | Lys | Ser | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Asp | Lys | Leu | Lys | Ile | Asn | Ile | Asp | Val | Leu | Phe | Pro | His | Met | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Cys | Ala | Tyr | Leu | Ser | Ile | Asp | Ala | Met | Asp | Val | Ala | Gly | Glu | Gln | Gln |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Asp | Val | Glu | His | Asn | Leu | Phe | Lys | Gln | Arg | Leu | Asp | Lys | Asp | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Pro | Val | Ser | Ser | Glu | Ala | Glu | Arg | His | Glu | Leu | Gly | Lys | Val | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro  
85 90

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
-15 -10 -5

Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg  
1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
50 55 60

Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
65 70 75 80

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys  
85 90 95

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala  
                  -15                  -10                  -5  
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val  
                  1                          5                  10  
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met  
          15                          20                          25  
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu  
          30                          35                          40                  45  
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala  
                  50                          55                          60  
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg  
                  65                          70                          75  
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile  
          80                          85                          90  
Ala Cys Lys Leu Cys  
          95

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.4  
seq PMLLRALAQAARA/GP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala  
-15 -10 -5  
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val  
1 5 10  
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met  
15 20 25  
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu  
30 35 40 45  
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa  
50 55 60  
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg  
65 70 75  
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile  
80 85 90  
Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile  
95 100 105  
Glu Ala Glu  
110

(2) INFORMATION FOR SEQ ID NO: 406:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(12) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(13) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq ILPLLFGCLGVFG/LF

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5 1 5 10
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
 15 20 25
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
 30 35 40
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
 45 50 55
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
 60 65 70 75
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
 80 85 90
Glu Ile Cys Ser
 95

```

## (2) INFORMATION FOR SEQ ID NO: 407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LLLVTWVFTPVT/ET

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
 -25 -20 -15
Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
 -10 -5 1
Ser Leu Asp Thr Glu Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 408:

## (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 63 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr  
-20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp  
1 5 10

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe  
15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg  
30 35 40

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.3  
seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

|           |           |           |           |            |           |     |           |           |            |            |           |           |           |           |            |
|-----------|-----------|-----------|-----------|------------|-----------|-----|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|
|           | -5        |           |           |            |           |     | 1         |           |            |            |           |           |           |           | 5          |
| Arg<br>10 | Ile       | Val       | Thr       | Ser        | Glu<br>15 | Glu | Val       | Ile       | Ile        | Arg<br>20  | Asp       | Ser       | Pro       | Val       | Leu<br>25  |
| Pro       | Val       | Thr       | Leu       | Gln<br>30  | Cys       | Asn | Leu       | Thr       | Ser<br>35  | Ser        | Ser       | His       | Thr       | Leu<br>40 | Thr        |
| Tyr       | Ser       | Tyr       | Trp<br>45 | Thr        | Lys       | Asn | Gly       | Val<br>50 | Glu        | Leu        | Ser       | Ala       | Thr<br>55 | Arg       | Lys        |
| Asn       | Ala       | Ser<br>60 | Asn       | Met        | Glu       | Tyr | Arg<br>65 | Ile       | Asn        | Lys        | Pro       | Arg<br>70 | Ala       | Glu       | Asp        |
| Ser       | Gly<br>75 | Glu       | Tyr       | His        | Cys       | Val | Tyr<br>80 | His       | Phe        | Val        | Ser<br>85 | Ala       | Pro       | Lys       | Ala        |
| Asn<br>90 | Ala       | Thr       | Ile       | Glu        | Val<br>95 | Lys | Ala       | Ala       | Pro        | Asp<br>100 | Ile       | Thr       | Gly       | His       | Lys<br>105 |
| Arg       | Ser       | Xaa       | Asn       | Lys<br>110 | Asn       | Glu | Gly       | Gln       | Asp<br>115 |            |           |           |           |           |            |

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION:  score 7.2
                        seq IMLLSLAAFSVIS/VV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met	Ala	Val	His	Asp	Leu	Ile	Phe	Trp	Arg	Asp	Val	Lys	Lys	Thr	Gly
	-35					-30					-25				
Phe	Val	Phe	Gly	Thr	Thr	Leu	Ile	Met	Leu	Leu	Ser	Leu	Ala	Ala	Phe
-20					-15					-10					-5
Ser	Val	Ile	Ser	Val	Val	Ser	Tyr	Leu	Ile	Leu	Ala	Leu	Leu	Ser	Val
				1				5					10		
Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Ser	Val	Ile	Gln	Ala	Val	Gln	Lys
		15					20					25			
Ser	Glu	Glu	Gly	His	Pro	Phe	Lys	Ala	Tyr	Leu	Asp	Val	Asp	Ile	Thr

30

35

40

Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His
 45 50 55 60

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (E) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro
 -30 -25 -20

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
 20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45

Val Met Val Ala Thr Asn Thr Pro Pro Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (E) LOCATION: -29..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
      -25                      -20                      -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
      -10                      -5                      1

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
      5                      10                      15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
      20                      25                      30                      35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa
      40                      45                      50

Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
      55                      60                      65

Phe
  
```

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (E) LOCATION: -32..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro
      -30                      -25                      -20

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
  
```

-15

-10

-5

Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10 15
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Xaa Val Gly Thr
 20 25 30
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
 35 40 45
 Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp
 50 55 60
 Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro
 65 70 75 80
 Lys Asp Ser Ile Gln Phe Ser Ser
 85

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LRLKLAATSASA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ala Leu Arg Leu Leu Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg
 -15 -10 -5 1
 Val Val Ala Ala Gly Ala Gln Arg Val Arg Gly Ile His Ser Ser Val
 5 10 15
 Gln Cys Lys Leu Arg Tyr Gly Met Trp His Phe Leu Leu Gly Asp Lys
 20 25 30
 Ala Ser Leu Arg Leu Thr Glu Arg Ser Arg Val Ile Thr Val Asp Gly
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

```

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                      -60                      -55                      -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
                      -45                      -40                      -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
                      -30                      -25                      -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
                      -15                      -10                      -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
   1                      5                      10                      15

Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
                      20                      25                      30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
                      35                      40                      45

Val Trp Lys Thr
                      50

```

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -154..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

```

Met Ala Leu Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
-150                               -145                               -140

Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr
-135                               -130                               -125

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
-120                               -115                               -110

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
-105                               -100                               -95

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
-90                               -85                               -80                               -75

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
-70                               -65                               -60

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
-55                               -50                               -45

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
-40                               -35                               -30

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
-25                               -20                               -15

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
-10                               -5                               1                               5

Lys Ala Thr

```

(x) INFORMATION FOR SEQ ID NO: 417:

1. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

2. MOLECULE TYPE: PROTEIN

3. ORIGINAL SOURCE:

(B) LOCATION: -70..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LAFSLPALPLAEL/QP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

```

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-70                               -65                               -60                               -55

Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
                               -50                               -45                               -40

Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
                               -35                               -30                               -25

Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
                               -20                               -15                               -10

Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
-5                               1                               5                               10

Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
                               15                               20                               25

Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
                               30                               35                               40

Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser
                               45                               50                               55

```

(2) INFORMATION FOR SEQ ID NO: 418:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(VI) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(1X) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.6
 seq KMVHLLVLSGAWG/MQ

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

```

Met Ala Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
                               -20                               -15                               -10

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val

```



```

      -5              1              5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
  10              15              20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
  25              30              35              40
Ala Phe Ile Asn Xaa Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
      45              50              55
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu
      60              65              70

```

(2) INFORMATION FOR SEQ ID NO: 419:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLLASGTTLFCTS/FY

(11) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```

Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala Leu Ser Gly
-60              -75              -70
Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Xaa Phe
-40              -60              -55              -50
Asp Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn Lys His His
      -45              -40              -35
Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys Arg Lys Pro
      -30              -25              -20
Trp Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu Phe Cys Thr
      -15              -10              -5
Tyr Tyr Gln Ala Gln

```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.5
 seq LLTLLPPPPPLYT/RH
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro
-20 -15 -10

Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro
-5 1 5 10

Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg
15 20 25

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -20..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.5
 seq ILFLLPSICSSNS/TG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys
-20 -15 -10 -5

Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val

				1				5						10					
Val	Thr	Thr	Thr	Xaa	Pro	Ser	Ile	Thr	Thr	Pro	Asn	Thr	Glu	Ser	Leu				
		15					20					25							
Gln	Lys	Asn	Val	Val	Thr	Pro	Thr	Thr	Gly	Thr	Thr	Xaa	Lys	Gly	Thr				
	30					35					40								
Ile	Thr	Asn	Glu	Leu	Leu	Lys	Met	Ser	Leu	Met	Ser	Thr	Ala	Xaa	Phe				
45					50					55					60				

(2) INFORMATION FOR SEQ ID NO: 422:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/OK

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met	Ala	Ser	Ser	Asn	Thr	Val	Leu	Met	Arg	Leu	Val	Ala	Ser	Ala	Tyr
				-15					-10					-5	
Ser	Ile	Ala	Gln	Lys	Ala	Gly	Met	Ile	Val	Arg	Arg	Val	Ile	Ala	Glu
			1				5					10			
Gly	Asp	Leu	Gly	Ile	Val	Glu	Lys	Thr	Cys	Ala	Thr	Asp	Leu	Gln	Thr
	15					20					25				
Lys	Ala	Asp	Arg	Leu	Ala	Gln	Met	Ser	Ile	Cys	Ser	Ser	Leu	Ala	Arg
	30				35					40					45
Pro	Ile	Pro	Lys	Leu	Thr	Ile	Ile	Gly	Glu	Glu	Asp	Leu	Pro	Ser	Glu
				50					55					60	
Asn	Val	Asp	Gln	Glu	Leu	Ile	Glu	Asp	Ser	Gln	Trp	Glu	Glu	Ile	Leu
			65					70					75		
Ile	Ile	Cys	Pro	Ser	Gln	Tyr	Ser	Ala	Ile	Lys	Glu	Glu	Asp	Leu	
	80					85					90				

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Arg Ser Ser Cys Val Leu Leu Thr Ala Leu Val Ala Leu Ala Ala
-15 -10 -5 1

Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser Val Ser Asp Pro Trp Lys
 5 10 15

Leu Met Leu Leu Asp Ala Thr Phe Arg Gly Ala Gln Gln Val Ser Asn
 20 25 30

Leu Ile His Tyr Leu Gly Leu Ser His His Leu Leu Ala Leu Asn Phe
 35 40 45

Ile Ile Val Ser Phe Gly Lys Lys Ser Ala Trp Ser Ser Ala Gln Val
 50 55 60 65

Lys Val Thr Asp Thr Asp Phe Asp Gly Val Glu Val Arg Val Phe Glu
 70 75 80

Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys Arg Ser Val Val Tyr Ile
 85 90 95

His Gly Xaa Gly Trp
 100

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -26..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35

Arg Phe Ala Leu Pro Thr Ala His His Met
40 45

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -69..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3
seq ILLIVLFLLDAYRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Thr Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile
-65 -60 -55

```

-35          -30          -25
Asn Lys Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu
-20          -15          -10
Asp Ala Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu
-5          1          5          10
Lys Ser Ser Thr Ser Arg Pro Arg
15

```

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq FLDFCVYIPLSWG/FC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

```

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
-85          -80          -75          -70
Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
-65          -60          -55
Glu Val Ser Gly Gly Pro Gly Gly Arg Arg Pro Phe Arg Pro Leu Ala
-50          -45          -40
Thr Glu Thr Phe Ser Leu Ala Val Gly Thr Phe Cys Ser Arg Glu Pro
-35          -30          -25
Val Gln Ser Asn Asn Leu His Leu Phe Leu Asp Phe Cys Val Tyr Ile
-20          -15          -10
Pro Leu Ser Trp Gly Phe Cys Pro Leu Gln Pro Ile Leu Ala
-5          1          5

```

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.2
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
-20 -15 -10

Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
-5 1 5

Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
10 15 20

Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
25 30 35 40

His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
45 50 55

Ala Arg Ala Asp Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa
60 65 70

Pro Phe Leu Cys Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro
75 80 85

Gly

(xii) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(D) OTHER INFORMATION: score 6.2
seq FLVSNMLLAEEYG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

```

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
  -20                      -15                      -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
  -5                      1                      5                      10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
          15                      20                      25

Trp Leu Asp Ala Gln Ser Gly
          30

```

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq SVLVLLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe His
  -40                      -35                      -30

Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu Val
  -25                      -20                      -15                      -10

Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys Ala
          -5                      1                      5

Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser Gln
          10                      15                      20

Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser Phe
          25                      30                      35

Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly Gln
          40                      45                      50                      55

```


Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met Leu
 60 65 70

Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val
 75 80 85

II INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VVXXSVLXTTCXS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala
 -75 -70 -65 -60

Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg
 -55 -50 -45

Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile
 -40 -35 -30

Asp Ala Gly Xaa Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val
 -25 -20 -15

Xaa Xaa Ser Val Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
 -10 -5 1

III INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LLAALMLVAMLQL/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```

Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr Gln Leu Leu Leu
  -25                      -20                      -15

Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu Tyr Leu Ser Leu
  -10                      -5                      1                      5

Leu Ser Gly Leu His Gly Pro
                10

```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```

Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val
      -15                      -10                      -5

Cys Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro
      1                      5                      10

Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr Ala Pro Met
      15                      20                      25

Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro Glu
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
-20 -15 -10
Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
-5 1 5 10
Leu Gln Cys Ser Val Gly Ile
15

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LMAFLLSFYLIPT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys

Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
-20 -15 -10 -5
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
1 5 10
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
15 20 25
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile
30 35 40

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr Ala Phe Ala
-20 -15 -10
Ser His Ile Arg Ala Arg Asp Ala Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.1
 seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Val His Lys Pro Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
      -20                      -15                      -10

His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
      -5                      1                      5

Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
      10                      15                      20

Thr Thr
      25
  
```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -28..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
      -25                      -20                      -15

Tyr Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
      -10                      -5                      1

Tyr Tyr Pro Thr
      4
  
```

(2) INFORMATION FOR SEQ ID NO: 438:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val
-20 -15 -10
Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr
-5 1 5 10
Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile
15 20 25
Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu
30 35 40
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln
45 50 55
Met Arg Asn Ser Gln Ala His Arg
60 65

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -87..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val

-85 -80 -75
 Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
 -70 -65 -60
 Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
 -55 -50 -45 -40
 Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
 -35 -30 -25
 Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
 -20 -15 -10
 Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Xaa
 -5 1 5
 Ser Leu Pro Ala Glu Pro Xaa Xaa Xaa Glu Asp Glu Ala Arg Glu Asn
 10 15 20 25
 Val Pro Pro

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq VTIILLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Val Thr Ile Ile Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys
 -10 -5 1
 Asn Val Thr Xaa Arg Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 441:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -87..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8
seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Xaa Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
   -85                      -80                      -75

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
   -70                      -65                      -60

Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile
-55                      -50                      -45                      -40

Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln
                      -35                      -30                      -25

Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala
   -20                      -15                      -10

Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser
   -5                      1                      5

Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn
  10                      15                      20                      25

Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His
   30                      35                      40

Glu Arg

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -89..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq DLSLLSLPPGTSP/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
-85 -80 -75
Pro Arg Val Ser Glu Leu Gln Val Leu Leu Gly Xaa Xaa Gly Arg Asn
-70 -65 -60
Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
-55 -50 -45
Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
-40 -35 -30
Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
-25 -20 -15 -10
Leu Ser Leu Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu
-5 1 5
Ala Pro Ile Pro Pro Thr Xaa Leu Ala Xaa Ala Xaa Cys Trp Ala Pro
10 15 20
Ser Val Arg Trp Thr Cys
25

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Pro Arg Ile Pro Xaa Leu Ala Thr Phe Arg Xaa Arg Ser Leu
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
 -35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
 -15 -10 -5

Cys Arg Cys Ala Gln Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp
 1 5 10

Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val
 15 20 25

Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu
 30 35 40 45

Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu
 50 55 60

Xaa Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn
 65 70 75

Gly Cys Thr Lys Ile Thr Xaa Ser Thr Cys
 80 85

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
-35 -30 -25 -20

Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
-15 -10 -5

Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp
1 5 10

Gly Ser Asn Trp Gln Gly
15

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -112..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq SSCILPWLSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Ala Ser Thr Phe Asp Glu His Asp Cys Glu Pro Ser Asp Pro Gln

Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val Asp Trp Asp His
 -80 -75 -70 -65
 His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu Asn Leu Pro Arg
 -60 -55 -50
 Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys Pro Val Cys Leu
 -45 -40 -35
 Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met Pro Cys His His
 -30 -25 -20
 Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser Lys Thr Asn Ser
 -15 -10 -5
 Cys Pro Leu Cys Arg Tyr Glu Leu Pro Thr Asp Asp Asp Thr Tyr Glu
 1 5 10 15
 Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln Gln His Arg Pro
 20 25 30

Xaa

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
 -15 -10 -5 1
 Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
 5 10 15
 Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln Pro Ser Pro
 20 25 30
 Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Gln Pro Arg
 35 40 45
 Pro Gly

50

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrernals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LRRLGCLTLTLS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Leu Gly Ile Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu
-70 -65 -60

Gly Leu Glu Gly Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly
-55 -50 -45

Ser Gly Gly Gly Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn
-40 -35 -30

Glu Ala Arg Gly Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu
-25 -20 -15 -10

Leu Gly Cys Leu Thr Leu Thr Leu Ser Gly Arg Ile
-5 1

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
  -15                      -10                      -5

Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
   1                      5                      10                      15

Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
                20                      25                      30

Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
                35                      40                      45

Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
                50                      55                      60

Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
   65                      70

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq AALPAWLSLQSRA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser Arg Ala
  -15                      -10                      -5

Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr Pro Val
   1                      5                      10                      15

Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg Pro Pro
                20                      25                      30

Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val Asp Gln
                35                      40                      45

```

Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro Ser Ala
 50 55 60
 Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly Val Pro
 65 70 75 80
 Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn Phe Leu
 85 90 95
 His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu Lys Asp
 100 105 110
 Phe Cys Thr Glu
 115

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
 -65 -60 -55 -50
 Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
 -45 -40 -35
 Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
 -30 -25 -20
 Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
 -15 -10 -5
 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
 1 5 10 15
 Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
 -45 -40 -35

Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val Ala Ala Thr
 -30 -25 -20

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
 -15 -10 -5

Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val Ile Val Leu
 -15 -10 -5

Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg Trp Gly Cys
 1 5 10

Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr Pro Asp Asn
 15 20 25 30

Phe Cys Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq VVFMVVAASGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu
 -25 -20 -15

Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe Ala Val
 -10 -5 1

Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro
 5 10 15

Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr
 20 25 30 35

Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg
 40 45 50

Val Thr

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LAHSLLLNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Glu Leu Ala His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln
-15 -10 -5 1
Ile Thr Glu Ala Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe
5 10 15
Leu Asp Lys Val Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys
20 25 30
Gln Lys Lys Leu Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro
35 40 45
Gly Pro Thr Gly
50

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
-25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
 -10 -5 1

Leu Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser
 5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys
 25 30 35

Arg Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser
 40 45 50

Gly Gln Arg Val Phe Val Val Lys Arg Gly
 55 60

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LVGVLFVSVTTG/PW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
 -30 -25 -20

Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
 -15 -10 -5 1

Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
 5 10 15

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn
 20 25 30

Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val
 35 40 45

Ser Lys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa Ser Gly Asn

Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa Xaa Val Ser
85 90 95
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys
100 105 110
Phe Gly Phe Val
115

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

```

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
      -10              -5                      1
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln
      5              10              15
Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
      20              25              30              35
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
      40              45              50
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
      55              60              65
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
      70              75              80
Glu Gln
      85

```

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -69..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq MMVLSLGIXLASA/SF

(iii) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

```

Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
      -65              -60              -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
      -50              -45              -40

```

Xaa Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10
 Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
 15 20 25
 Ile Ser Gly Ser Leu Ser Ile
 30

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Xaa Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Xaa Leu Ile Thr Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val Thr Trp Phe Leu
 105 110

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```
Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
-25                -20                -15                -10

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
      -5                        1                        5

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
    10                15                20

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
    25                30                35

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
    40                45                50                55

Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
      60                65                70

Gln Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
    75                80                85

Asp Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
    90                95                100

Thr Phe Val His Val Val Pro
    105                110
```

(2) INFORMATION FOR SEQ ID NO: 463:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AIALATVLFLLGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```

Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
   -55                      -50                      -45

Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
  -40                      -35                      -30

Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 -25                      -20                      -15                      -10

Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
      -5                      1                      5

Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
    10                      15                      20

Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
    25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp

```



```

-15          -10          -5          1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
          5          10          15
Gln His Pro Thr Xaa Gln
          20

```

(2) INFORMATION FOR SEQ ID NO: 465:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15 -10 -5 1

Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
5 10 15

Gln His Pro Thr Gln Cys Ser Thr His Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 466:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(U) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

```

Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
      -65                      -60                      -55

Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
      -50                      -45                      -40

Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      -35                      -30                      -25

Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
      -20                      -15                      -10                      -5

His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
              1              5              10

Ala

```

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -94..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VILQLQFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```

Met Phe Gly Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln
      -90                      -85                      -80

Arg Asp Ser Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly
      -75                      -70                      -65

Asp Val Val Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr
      -60                      -55                      -50

Leu Gln Gln Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly
      -45                      -40                      -35

Pro Gly Gln Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser

```

-30	-25	-20	-15
Pro Val Ile Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr			
-10	-5	1	
Leu Ser Leu Lys Leu Val His Val Ala Gly Pro Gly Pro Thr			
5	10	15	

(1) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILVGTSKHVAFG/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu		
-85	-80	-75
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly		
-70	-65	-60
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp		
-50	-45	-40
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu		
-35	-30	-25
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser		
-20	-15	-10
Lys His Val Ala Phe Gly Lys Ile Ile		
-5	1	

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq WYSTVGLLPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys Asp His Gly Thr
-35                               -30                     -25           -20

Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly Leu Leu Pro Pro
                        -15                     -10           -5

Val Arg Ala Met Ser Gln Arg Asn Leu Asn
          1                      5

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Ala Ala Ala Leu Lys Cys Leu Leu Thr Leu Gly Arg Trp Cys Pro
-35                               -30                     -25

Gly Leu Gly Val Ala Pro Gln Ala Arg Ala Leu Ala Ala Leu Val Pro
-20                               -15                     -10           -5

Gly Val Thr Gln Val Asp Asn Lys Ser Gly Phe Leu Gln Lys Arg Pro
          1                      5                      10

His Arg Gln His Pro Gly Ile Leu Lys Leu Pro His Val Arg Leu Pro
      15                      20                      25

```

Gln Ala Leu Ala Asn Gly Ala Gln Leu Leu Leu Gly Ser Ala Gly
 30 35 40

Pro Thr Met Glu Asn Gln Val Gln Thr Leu Thr Ser Tyr Leu Trp Ser
 45 50 55 60

Arg His Leu Pro Val Glu Pro Xaa Glu Leu Gln Arg Arg Ala Xaa His
 65 70 75

Leu Glu Lys Lys Phe Leu Glu Asn Pro Asp Leu Ser Gln Thr Glu Glu
 80 85 90

Lys Leu Arg Gly Ala Gly
 95

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -102..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu Ile Lys Gly Ser
 -100 -95 -90

Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly
 -85 -80 -75

Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val
 -70 -65 -60 -55

His His Ala Met Xaa Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly
 -50 -45 -40

Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile
 -35 -30 -25

Arg Arg Ser Trp Xaa Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser

Val Lys Ala Leu Gly
15

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Val Asn Glu Leu Gln Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala
-15 -10 -5

Cys Ser Ser Ser Lys Gln Arg Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FFFSIQPFLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala Phe Phe Phe Ser Ile

```

                -20                -15                -10
Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu Lys Ser Pro Ser Pro
      -5                        1                        5
Val Ala His Pro Thr Asn Ile Ser Val Ser Glu Asn Ala Gln Arg Cys
      10                        15                        20
Leu Xaa Thr Ser Pro Trp
      25                        30

```

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WVIVLTSWITIFQ/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

```

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
      -75                        -70                        -65
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
      -60                        -55                        -50
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
      -45                        -40                        -35
Gln Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
      -30                        -25                        -20
Leu Asn Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
      -15                        -10                        -5                        1
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile
      5                        10                        15
Leu Gly Thr Pro Asp Asn Phe Cys Phe Tyr
      20                        25

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
-70 -65 -60 -55

Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
 -50 -45 -40

Gly Arg Glu Ala Met Ala Ser Gly Ser Asn Trp Leu Ser Gly Val Asn
 -35 -30 -25

Val Val Leu Val Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe
 -20 -15 -10

Ile Phe Val Lys Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg
 -5 1 5 10

Gly Pro His Val Pro Val Gly Xaa Gln Cys Pro Gln Xaa Cys Tyr Asn
 15 20 25

Tyr Leu Tyr

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9

seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
-55                      -50                      -45

Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser
-40                      -35                      -30                      -25

Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
-20                      -15                      -10

Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly
-5                      1                      5

Pro Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro
10                      15                      20

Phe Val
25

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Ala Glu Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys
-25                      -20                      -15

Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
-10                      -5                      1                      5

Ser Thr Arg Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser

```

Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LXXVVAFVAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Val Arg Arg Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu
 -15 -10 -5

Ser Gln Gln Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly
 1 5 10 15

Gln Glu Arg Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly
 20 25 30

Asp Cys Gln Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp
 35 40 45

Gly Ser Asp Val Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys
 50 55 60

Thr Lys Glu Ala Gly Asp Gly Pro Leu
 65 70

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq PIVRLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

```

Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn Leu Cys Ala
  -35                      -30                      -25

Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu Leu Ser Cys
  -20                      -15                      -10

Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln Pro Ser Gly
  -5                      1                      5                      10

Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg Arg Phe Ser
      15                      20                      25

Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr Val Leu Ile
      30                      35                      40

His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys Tyr Leu Ser
      45                      50                      55

Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser Phe Gly Leu
      60                      65                      70                      75

Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly Ser Leu Gln
      80                      85                      90

Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala Ile Pro Phe
      95                      100                      105

Arg Ser Arg Ser Ser
      110

```

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg
-60                -55                -50                -45

Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly
                -40                -35                -30

Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu
                -25                -20                -15

Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val
                -10                -5                1

Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys
  5                10                15                20

Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Xaa
                25                30                35

Asn Met Asn Leu Glu Gly Gly
                40

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly Asp Ser Gly
                -30                -25                -20

Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn Gln Val Leu
                -15                -10                -5

Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His
  1                5                10                15

Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu
                20                25                30

```

Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr
 35 40 45
 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa Val His Asp
 50 55 60
 Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp Ser Leu Glu
 65 70 75
 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val
 80 85 90

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly
 -30 -25 -20
 Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu
 -15 -10 -5 1
 Trp Leu Leu Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile
 5 10 15
 Gln Phe Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg
 20 25 30
 Leu Met Ile Arg Lys Leu Val Ala Glu Asn Arg
 35 40

INFORMATION FOR SEQ ID NO: 483:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Surrenals

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -26..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
25 30 35

Cys Ala Arg
40

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys
-30 -25 -20

Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala

```

-15              -10              -5              1
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
          5              10              15
Ser Val Leu Lys Leu His His Ser Arg Gly
      20              25

```

(2) INFORMATION FOR SEO ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq SLAAALTLGHWG/LG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Asp Tyr Ser Leu Ala Ala Ala Leu Thr Leu His Gly His Trp Gly
-15 -10 -5

Leu Gly Gln Val Val Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO: 486:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

11. MOLECULE TYPE: PROTEIN

ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq LSLXASYIFGISG/FE

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
  -70                      -65                      -60

Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
  -55                      -50                      -45

Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
  -40                      -35                      -30                      -25

Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
          -20                      -15                      -10

Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
          -5                      1                      5

Arg Asn Glu Phe Val Arg Gln Ser
  10                      15
  
```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
  -75                      -70                      -65

Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
  -60                      -55                      -50                      -45

Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
          -40                      -35                      -30

Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Xaa Leu
  -25                      -20                      -15
  
```


Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVCLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Trp Phe Glu Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu
 -20 -15 -10

Leu Ile Pro Gly Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg
 -5 1 5 10

Gly Lys Glu Lys Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met
 15 20 25

Thr Arg Asp Arg Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys
 30 35 40

Gly
 45

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Glu Phe Lys Leu Glu Ala His Arg Ile Val Ser Ile Ser Leu Gly
 -45 -40 -35
 Lys Ile Tyr Asn Ser Arg Val Gln Arg Gly Gly Ile Lys Leu His Lys
 -30 -25 -20 -15
 Asn Leu Leu Val Ser Leu Val Leu Arg Xaa Pro Ala Lys Ser Thr Arg
 -10 -5 1
 Ala Gly

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain

(iii) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -97..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq IASGLGLXLDWCWT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
 -95 -90 -85
 Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
 -80 -75 -70
 Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
 -65 -60 -55 -50
 Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
 -45 -40 -35
 Leu Glu Val Tyr Pro Xaa Phe Leu Phe Phe Leu Ala Val Gly Gly Val
 -30 -25 -20
 Phe His Pro Arg Ile Ala Ser Gly Leu Gly Leu Xaa Leu Asp Cys Trp
 -15 -10 -5

Thr Ser Ser Leu Cys Leu Trp Leu Leu His Gly Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq RIPSPLPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala
-40 -35 -30
Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro
-25 -20 -15
Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
 -15 -10 -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
 1 5 10 15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
 20 25 30

Ala Arg Thr
 35

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq FLLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe Leu Leu Leu
 -25 -20 -15 -10

Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -77..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
   -75                      -70                      -65

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
   -60                      -55                      -50

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
   -45                      -40                      -35                      -30

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
                   -25                      -20                      -15

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
   -10                      -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```
Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys
   -20                      -15                      -10

Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly
   1                      5                      10

Met Tyr Tyr Arg Gly Gly Val
```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -25..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LVFMVPLVGLIHL/GW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
-25 -20 -15 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
 10 15 20

Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 497:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Spleen
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -23..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq VFCLLISIPTPSA/HL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Gly Trp Asp Gly Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile

-20

-15

-10

Ser Ile Pro Thr Pro Ser Ala His Leu
 -5 1

(C) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILAHLGLIPIHA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met	Ala	Ala	Ser	Gln	Ala	Val	Glu	Glu	Met	Arg	Thr	Ala	Trp	Phe	Trp	-115	-110	-105	
Gly	Ser	Leu	Gly	Phe	Ala	Met	Ser	Ile	Leu	Leu	Thr	Phe	Pro	Val	Thr	-100	-95	-90	
Ile	Pro	Val	Met	Met	Met	Pro	Gly	Thr	Arg	Xaa	Gly	Phe	Glu	Xaa	Arg	-85	-80	-75	
Xaa	Phe	Arg	Val	Asp	Val	Val	His	Met	Asp	Glu	Asn	Ser	Leu	Glu	Phe	-70	-65	-60	-55
Asp	Met	Val	Gly	Ile	Asp	Ala	Ala	Ile	Ala	Asn	Ala	Phe	Arg	Arg	Ile	-50	-45	-40	
Leu	Leu	Ala	Glu	Val	Pro	Thr	Met	Ala	Val	Glu	Lys	Val	Leu	Val	Tyr	-35	-30	-25	
Asn	Asn	Thr	Ser	Ile	Val	Gln	Asp	Glu	Ile	Leu	Ala	His	Arg	Leu	Gly	-20	-15	-10	
Leu	Ile	Pro	Ile	His	Ala	Asp	Pro	Arg	Leu	Phe	Glu	Tyr	Arg	Asn	Gln	-5	1	5	10
Ala	Arg	Gln	Thr	Gly	Thr	Glu	Ile	Asp	Thr	Leu	Gln	Phe	Arg	Leu	Gln				

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -77..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq FEARIALLPLLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
   -75                      -70                      -65

Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
   -60                      -55                      -50

Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
   -45                      -40                      -35                      -30

Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
          -25                      -20                      -15

Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
          -10                      -5                      1

Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
   5                      10                      15

Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa Xaa Val Pro
   20                      25                      30                      35

His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
          40                      45

```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLFFTGWIIIDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp
-40 -35 -30
Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe
-25 -20 -15
Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr
-10 -5 1 5
Arg

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -44..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Met Thr Ala Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg
-40 -35 -30
Ile Ile Cys Ser Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu
-25 -20 -15
Val Ser Thr Thr Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq FLTALLWRGRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

```

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
      -10                -5                      1

Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
      5                  10                      15

Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
    20                25                      30

Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
    35                40                45                50

Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
    55                60                65

Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Xaa
    70                75                80

Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
    85                90                95

Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
   100                105                110

Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
   115                120                125

```

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

```
Met Asn Gln Glu Asn Pro Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala
-90                               -85                               -30                               -75

Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly
                               -70                               -65                               -60

Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln
                               -55                               -50                               -45

Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr
                               -40                               -35                               -30

Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu
-25                               -20                               -15

Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp
-10                               -5                               1
```

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3

```

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu
      -50              -45              -40
Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val Leu Leu Pro
      -35              -30              -25
Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp Leu Leu Val
      -20              -15              -10
Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
      -5              1              5              10
Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
      15              20              25
Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
      30              35              40
Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys His Arg Xaa
      45              50              55
Leu His His Tyr Tyr Gly Cys
      60              65

```

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu Pro
      -10              -5              1
Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys Lys
      5              10              15
Ala Arg Ser
      20

```

(2) INFORMATION FOR SEQ ID NO: 506:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 -15 -10 -5
Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
 1 5 10
Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
15 20 25
Ile Ser Arg Leu Arg
30

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLLXRVSVTAVAA/LS

-15 -10 -5
 Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa Leu Gly Phe Gly Gly Phe
 1 5 10 15
 Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala Pro Val Arg His Ser Gly
 20 25 30
 Asp His Gly Lys Arg Leu Phe Val Ile Arg Pro Ser Arg Phe Tyr Asp
 35 40 45
 Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr Ile Ala Leu Thr Gly Ile
 50 55 60
 Pro Val Ala Xaa Phe Ile Thr Leu Val Asn Val Phe Ile Gly Gln Ala
 65 70 75
 Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val Pro Glu His Trp Glu Tyr
 80 85 90 95
 Tyr Lys His Pro Ile Ser Arg Trp Ile Ala Arg Asn Phe Tyr Asp Ser
 100 105 110
 Pro Xaa Lys Ile Tyr Glu Arg Thr Met
 115 120

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu
 -25 -20 -15 -10
 Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly
 -5 1 5
 Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys
 10 15 20
 Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg

25 30 35
 Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys
 40 45 50 55
 Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu
 60 65 70
 Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro
 75 80 85
 Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr
 90 95 100
 Ile Ala Pro
 105

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val Glu Met Val Gln Ala
 -40 -35 -30
 Leu Tyr Gln Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile
 -25 -20 -15 -10
 Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr Tyr Lys Leu Gln Glu
 -5 1 5
 Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp
 10 15 20
 Leu Ile His Pro Leu Val Pro Pro Val Pro Lys Asp His Pro Ala Leu

Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu
 60 65 70

Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala Ser Leu Lys Lys Tyr
 75 80 85

Gly Val Gly Thr Cys Gly Pro Cys
 90 95

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCARS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro
 -75 -70 -65

Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50

Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Xaa
 -45 -40 -35

Xaa Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20

Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 -15 -10 -5 1

Pro Ser

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
-30 -25 -20
Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
-15 -10 -5
Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
1 5 10 15
His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
20 25 30
Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser
35 40 45
Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln
50 55 60
Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys Tyr
65 70 75 80
Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly Xaa
85 90 95
Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly
100 105 110

(x) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(E) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(D) OTHER INFORMATION: score 4.1
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
-55 -50 -45
Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr Gly
-40 -35 -30
Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
-25 -20 -15
His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
-10 -5 1 5
Ala Tyr Leu Pro Thr Gly Lys Trp
10

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Ala Thr Leu Thr Phe Ser Leu Arg Lys Pro Leu Gln Arg Ser Leu
-85 -80 -75
Ile Arg Pro Ser His Leu Pro Leu Cys Cys Phe Asp Trp Arg Leu Ser
-70 -65 -60
His Tyr Tyr Arg Leu Pro Pro Ala Val Arg Leu His Gln Gln Arg Gly
-55 -50 -45
Gly Arg Pro Gly Arg Ser Ser Ala Asp His Trp His Ser Gly Val Pro
-40 -35 -30 -25
Thr Arg Ile Leu Pro Pro Ala His Arg Leu Leu Cys Ile Gln Arg Leu
-20 -15 -10

Pro Trp Leu Leu Leu Cys Arg Gly Ile Thr Ser
 -5 1

(ii) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
 seq PSLAAGLLFGSXA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 -45 -40 -35

Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
 -30 -25 -20

Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Xaa
 -15 -10 -5

Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
 1 5 10 15

Gly Phe Leu Ala Ala Thr Ser Val
 20

(ii) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly
   -15                -10                -5

Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln
    1                5                10

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
   15                20                25                30

Tyr Tyr Arg Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala
    35                40                45

Gly
  
```

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -83..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

```

Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
   -80                -75                -70

Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
   -65                -60                -55

Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
   -50                -45                -40

Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Val Gln Gly Pro
  -35                -30                -25                -20

His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg Leu Leu Ser Gln
   -15                -10                -5
  
```

Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe Ser Gln Tyr Cys
 1 5 10
 Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe Phe Phe
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ITSSLFLGRGSVA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala Pro
 -40 -35 -30
 Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr Ser
 -25 -20 -15
 Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu Leu
 -10 -5 1 5
 Gln Ala Arg Gly Ile
 10

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

```

Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly Thr
    -15                      -10                      -5

Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe Leu
    1                      5                      10

Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser Asp
    15                      20                      25                      30

Phe Glu Lys Val Gln Glu Arg
    35
  
```

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

```

Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly
    -15                      -10                      -5

Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Thr
    1                      5                      10

Leu
  
```

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq MLLSIGMLMLSAT/QV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
-10 -5 1
Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
5 10 15
Glu Xaa Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
20 25 30 35
Asp Asp Leu Pro Ala Arg Phe Gly Tyr
40

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Leu Thr Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-5 -20 -15 -10

Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
 25 30 35

Xaa Xaa Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
 40 45 50 55

Pro Phe Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
 -60 -55 -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
 -45 -40 -35 -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
 -25 -20 -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
 -10 -5 1

Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5 10 15

Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn Gly Arg
 20 25 30 35

Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
 40 45

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Ala Ile Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser
-30 -25 -20 -15

Lys Leu Trp Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile
-10 -5 1

Xaa Ala Glu Pro Pro Gln Leu Asp Ile Ser
5 10

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FVLGSARLGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu Asp Asp Phe Val
-20 -15

10

15

20

Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg Val Arg Thr Ala
25 30 35

Thr

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Lys Leu Val Ser Ala Thr Ala Trp Leu Glu Glu Cys Trp Trp Ser
-15 -10 -5 1

Glu Leu Ser

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LYVPLLAVCCLHS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu Leu Trp
 -30 -25 -20

Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys Cys Leu
 -15 -10 -5

His Ser Val Val Phe Phe
 1

(2) INFORMATION FOR SEQ ID NO: 527:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -118..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LMIALTUVGCI FM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
 -115 -110 -105

Leu Cys Glu Arg Asp Val Ser Xaa Ser Leu Arg Leu Thr Arg Ser Ser
 -100 -95 -90

Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
 -85 -80 -75

Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
 -7 -65 -60 -55

Arg Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
 -50 -45 -40

Xaa Xaa Ile Pro Glu Thr Val Ser Leu Glu Met Leu Xaa Xaa Ala Lys
 -35 -30 -25

Asn Lys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val
 -20 -15 -10

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -100..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGGLG/FI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100                      -95                      -90                      -85

Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
                      -80                      -75                      -70

Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
                      -65                      -60                      -55

Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50                      -45                      -40

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35                      -30                      -25

Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20                      -15                      -10                      -5

Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile
                      1                      5                      10

Pro Lys Leu Asn Arg Phe
                      15

```

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq MLVLRSGLTALA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr
-10 -5 1
Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val Arg Lys Ala
5 10 15
Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile Pro Asn Leu
20 25 30 35
Ala Arg Ile Asp Lys Gln Glu Thr Arg
40

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq NIESLAWTGGTLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Ala Ala Pro Leu Ser Val Glu Val Glu Phe Gly Gly Gly Ala Xaa
-35 -30 -25
Ser Lys Leu Thr Val Leu Arg Asn Ile Glu Ser Leu Ala Trp Thr Gly
-15 -10 -5

15

20

25

Arg Asn Ser Gly Ala Asp Tyr Arg
30 35

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Thr His Leu Ile Glu Tyr Asp Arg His Arg Lys Ser Arg Leu Ser
-65 -60 -55 -50
Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp His Ser Arg Asn Ala
-45 -40 -35
Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro Pro Thr Val Asp Ser
-30 -25 -20
Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val Ile Phe Trp Ser Trp
-15 -10 -5
Ala Gly Leu Val
1

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -22...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ala Ala Ala Ala Leu Gly Gln Ile Trp Ala Arg Lys Leu Leu Ser
-20 -15 -10
Val Pro Trp Leu Leu Cys Gly Pro Arg Arg Tyr Ala Ser Ser Ser Phe
-5 1 5 10
Lys Ala Ala Asp Leu Gln Leu Glu Met Thr Gln Lys Pro His Lys Lys
15 20 25
Pro Gly Pro Gly Glu Pro Leu Val Phe Gly Lys Thr Phe Thr Asp His
30 35 40
Met Leu Met Val Glu Trp Asn Asp Lys Gly Trp Gly Gln Pro Arg Ile
45 50 55
Gln Pro Phe Gln Asn Leu Thr Leu His Pro Ala Ser Ser Ser Leu His
60 65 70
Tyr Ser Leu Gln Leu Phe Glu Gly
75 80

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -38...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ala Val Val Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg
 -5 1 5 10
 Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala
 15 20 25
 Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala
 30 35 40
 Arg Xaa Lys Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val
 45 50 55
 Lys Arg Pro
 60

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPHTA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 -5 1 5 10
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met
 15 20 25
 Pro Leu Ser Asp Val Leu
 30

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -86..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
-85 -80 -75
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
-70 -65 -60 -55
Lys Leu Xaa Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
-50 -45 -40
Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
-35 -30 -25
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
-20 -15 -10
Thr Ala Val Thr Ser Gly Arg Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -68..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq ILLGNYCVAVADA/KK

-65 -60 -55
 Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu
 -50 -45 -40
 Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr
 -35 -30 -25
 Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala
 -20 -15 -10 -5
 Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr
 1 5 10
 Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala
 15 20 25
 Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
 30 35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly Tyr Ala Gln Glu Asp
 -60 -55 -50 -45
 Arg Glu Arg Met His Arg Asn Ile Val Ser Leu Ala Gln Asn Leu Leu
 -40 -35 -30
 Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp
 -25 -20 -15
 Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro
 -10 -5 1
 Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu Asn Ala Ala Trp Pro
 5 10 15 20

Arg

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (E) OTHER INFORMATION: score 3.5
seq WSPLSTRSGGTHA/CS

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
-30 -25 -20

Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys
-15 -10 -5 1

Ser Ala Ser Met Arg Gln Pro Trp
5

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (B) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (E) OTHER INFORMATION: score 3.5

```

Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
      -50                -45                -40

Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
      -35                -30                -25

Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
      -20                -15                -10

Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
      -5                1                5                10

Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
      15                20                25

Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
      30                35                40

Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr Thr Val Arg
      45                50                55

```

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq GLVCAGLADMARPAE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```

Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
      -60                -55                -50

Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
      -45                -40                -35

Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
      -30                -25                -20

Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
      -15                -10                -5                1

Glu Lys Leu Ser Thr Ala Gln Ser Xaa Val Leu Met Ala Thr Gly Phe
      5                10                15

```

Ile Trp Ser Arg Tyr Ser
20

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -86..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TGXLNMTLQRASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Met	Ser	Asn	Tyr	Ser	Val	Ser	Leu	Val	Gly	Pro	Ala	Pro	Trp	Gly	Phe	-85	-80	-75	
Arg	Leu	Gln	Gly	Gly	Lys	Asp	Phe	Asn	Met	Pro	Leu	Thr	Ile	Ser	Ser	-70	-65	-60	-55
Leu	Lys	Asp	Gly	Gly	Lys	Ala	Ala	Gln	Ala	Asn	Val	Arg	Ile	Gly	Asp	-50	-45	-40	
Val	Val	Leu	Ser	Ile	Asp	Gly	Ile	Asn	Ala	Gln	Gly	Met	Thr	His	Leu	-35	-30	-25	
Glu	Ala	Gln	Asn	Lys	Ile	Lys	Gly	Cys	Thr	Gly	Xaa	Leu	Asn	Met	Thr	-20	-15	-10	
Leu	Gln	Arg	Ala	Ser	Ala	Ala	Pro	Lys	Pro	Glu	Pro	Val	Pro	Val	Gln	-5	1	5	10
Lys	Pro	Thr	Val	Thr	Ser	Val	Cys	Ser	Glu	Thr	Ser	Gln	Glu	Leu	Ala	15	20	25	
Glu	Gly	Gln	Arg	Arg	Gly	Ser	Gln	Gly	Asp	Ser	Lys	Gln	Gln	Asn	30	35	40		

(2) INFORMATION FOR SEQ ID NO: 542:

SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
-15 -10 -5

Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
1 5 10

Lys Glu Leu Gln Gln
15

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -40..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq ALLCTLLLLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ile Ile Pro Leu Leu Glu Ile Leu Ile Ile Ile Val Leu Asn Glu
-40 -35 -30 -25

Val Leu Leu Phe Asp Val Asn Ser Val Tyr Lys Ala Leu Leu Cys Thr
-20 -15 -10

Leu Leu Leu His Phe Gln Asn Ile Arg Arg Phe Leu Ser Ser Gln Ser
-5 1 5

Pro Met Lys Ala Val Ser Leu Leu Xaa Phe His Gln Pro Asp Phe Asp

10

15

20

Tyr Ile
25

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro Pro Ser Ala Thr Pro
   -50                      -45                      -40

Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His Ser Thr Ala Arg Ile
   -35                      -30                      -25

Val Met Pro Leu His Tyr Ser Leu Val Phe Ile Ile Gly Leu Val Gly
  -20                      -15                      -10                      -5

Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn Arg Lys Lys Ile Asn
      1                      5                      10

Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile Ser Asp Ile Leu Phe
      15                      20                      25

Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met Xaa Trp Ala Leu Thr
      30                      35                      40

Asn Glu Ser Glu Met Trp
      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Pancreas

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -29..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser
-25 -20 -15

Ser Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile
-10 -5 1

Gln Gln Arg
5